



## SEQUENCE LISTING

<110> Hitoshi, Yasumichi  
Jenkins, Yonchu  
Markovtsov, Vadim  
Rigel Pharmaceuticals, Inc.

<120> Modulators of Cellular Proliferation

<130> 021044-004010US

<140> US 10/620,052

<141> 2003-07-14

<150> US 60/395,443

<151> 2002-07-12

<160> 78

<170> PatentIn Ver. 2.1

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protein kinase C isoform

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protein kinase C isoform

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<223> phosphoinositide-specific phospholipase C beta 1,  
isoform a (PLC-beta1), transcript variant 1

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isoform a (PLC-beta1), transcript variant 1

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			980					985					990			
Asp	Leu	Ala	Ala	Leu	Asp	Ala	Glu	Met	Thr	Gln	Lys	Leu	Ile	Asp	Leu	
		995				1000						1005				
Lys	Asp	Lys	Gln	Gln	Gln	Gln	Leu	Leu	Asn	Leu	Arg	Gln	Glu	Gln	Tyr	
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Tyr	Ser	Glu	Lys	Tyr	Gln	Lys	Arg	Glu	His	Ile	Lys	Leu	Leu	Ile	Gln	
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Lys	Leu	Thr	Asp	Val	Ala	Glu	Glu	Cys	Gln	Asn	Asn	Gln	Leu	Lys	Lys	
				1045					1050					1055		
Leu	Lys	Glu	Ile	Cys	Glu	Lys	Glu	Lys	Lys	Glu	Leu	Lys	Lys	Lys	Met	
			1060					1065					1070			
Asp	Lys	Lys	Arg	Gln	Glu	Lys	Ile	Thr	Glu	Ala	Lys	Ser	Lys	Asp	Lys	
		1075					1080					1085				
Ser	Gln	Met	Glu	Glu	Glu	Lys	Thr	Glu	Met	Ile	Arg	Ser	Tyr	Ile	Gln	
		1090				1095					1100					



Glu Val Val Gln Tyr Ile Lys Arg Leu Glu Glu Ala Gln Ser Lys Arg  
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<210> 5

<211> 3052

<212> DNA

<213> Homo sapiens

<220>

<223> cytoplasmic tyrosine kinase focal adhesion kinase  
(FAK)

<400> 5

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<210> 6

<211> 879

<212> PRT

<213> Homo sapiens

<220>

<223> cytoplasmic tyrosine kinase focal adhesion kinase  
(FAK)

<400> 6

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Ser Val Lys Ala Lys Thr Leu Arg Lys Leu Ile Gln Gln Thr Phe Arg
          35                      40                      45

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Gln Phe Ala Asn Leu Asn Arg Glu Glu Ser Ile Leu Lys Phe Phe Glu
          50                      55                      60

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Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys Glu Cys Phe Lys Cys Ala
          65                      70                      75                      80

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```

Leu Gly Ser Ser Trp Ile Ile Ser Val Glu Leu Ala Ile Gly Pro Glu
          85                      90                      95

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Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly Cys Asn Pro Thr His Leu
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Ala Asp Phe Thr Gln Val Gln Thr Ile Gln Tyr Ser Asn Ser Glu Asp
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Lys Asp Arg Lys Gly Met Leu Gln Leu Lys Ile Ala Gly Ala Pro Glu
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Phe	Ile	Ile	Arg	Pro	Gln	Lys	Glu	Gly	Glu	Arg	Ala	Leu	Pro	Ser	Ile	180	185	190	
Pro	Lys	Leu	Ala	Asn	Ser	Glu	Lys	Gln	Gly	Met	Arg	Thr	His	Ala	Val	195	200	205	
Ser	Val	Ser	Glu	Thr	Asp	Asp	Tyr	Ala	Glu	Ile	Ile	Asp	Glu	Glu	Asp	210	215	220	
Thr	Tyr	Thr	Met	Pro	Ser	Thr	Arg	Asp	Tyr	Glu	Ile	Gln	Arg	Glu	Arg	225	230	235	240
Ile	Glu	Leu	Gly	Arg	Cys	Ile	Gly	Glu	Gly	Gln	Phe	Gly	Asp	Val	His	245	250	255	
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Gln	Glu	Ala	Cys	His	Tyr	Thr	Ser	Leu	His	Trp	Asn	Trp	Cys	Arg	Tyr	290	295	300	
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Leu	Thr	Met	Arg	Gln	Phe	Asp	His	Pro	His	Ile	Val	Lys	Leu	Ile	Gly	325	330	335	
Val	Ile	Thr	Glu	Asn	Pro	Val	Trp	Ile	Ile	Met	Glu	Leu	Cys	Thr	Leu	340	345	350	
Gly	Glu	Leu	Arg	Ser	Phe	Leu	Gln	Val	Arg	Lys	Tyr	Ser	Leu	Asp	Leu	355	360	365	
Ala	Ser	Leu	Ile	Leu	Tyr	Ala	Tyr	Gln	Leu	Ser	Thr	Ala	Leu	Ala	Tyr	370	375	380	
Leu	Glu	Ser	Lys	Arg	Phe	Val	His	Arg	Asp	Ile	Ala	Ala	Arg	Asn	Val	385	390	395	400
Leu	Val	Ser	Ser	Asn	Asp	Cys	Val	Lys	Leu	Gly	Asp	Phe	Gly	Leu	Ser	405	410	415	
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Pro	Ile	Lys	Trp	Met	Ala	Pro	Glu	Ser	Ile	Asn	Phe	Arg	Arg	Phe	Thr	435	440	445	
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Pro	Thr	Leu	Tyr	Ser	Leu	Met	Thr	Lys	Cys	Trp	Ala	Tyr	Asp	Pro	Ser	500	505	510	
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Arg	Ser	Gln	Glu	Ile	Ala	Met	Trp	Gln	Pro	Asn	Val	Glu	Asp	Ser	Thr	625	630	635	640
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Glu	Glu	Arg	Leu	Ile	Arg	Gln	Gln	Gln	Glu	Met	Glu	Glu	Asp	Gln	Arg	660	665	670	
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Gln	Pro	Val	Gly	Lys	Pro	Asp	Pro	Ala	Ala	Pro	Pro	Lys	Lys	Pro	Pro	690	695	700	
Arg	Pro	Gly	Ala	Pro	Gly	His	Leu	Gly	Ser	Leu	Ala	Ser	Leu	Ser	Ser	705	710	715	720
Pro	Ala	Asp	Ser	Tyr	Asn	Glu	Gly	Val	Lys	Leu	Gln	Pro	Gln	Glu	Ile	725	730	735	
Ser	Pro	Pro	Pro	Thr	Ala	Asn	Leu	Asp	Arg	Ser	Asn	Asp	Lys	Val	Tyr	740	745	750	
Glu	Asn	Val	Thr	Gly	Leu	Val	Lys	Ala	Val	Ile	Glu	Met	Ser	Ser	Lys	755	760	765	
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Gly Leu Ala Leu Arg Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro  
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 Leu Leu Pro Ala Ser Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu  
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 Leu Asn Ser Asp Leu Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln  
 820 825 830  
 Gln Tyr Val Met Thr Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu  
 835 840 845  
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<210> 7

<211> 4089

<212> DNA

<213> Homo sapiens

<220>

<223> calcium dependent tyrosine kinase focal adhesion  
kinase 2 (FAK2)

<400> 7

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<210> 8

<211> 1009

<212> PRT

<213> Homo sapiens

<220>

<223> calcium dependent tyrosine kinase focal adhesion  
kinase 2 (FAK2)

<400> 8

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35 40 45

Ser Phe Asn Pro Gly Lys Asn Phe Lys Leu Val Lys Cys Thr Val Gln  
50 55 60

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Tyr	Asp	Leu	Gln	Ile	Arg	Tyr	Leu	Pro	Glu	Asp	Phe	Met	Glu	Ser	Leu	
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 (CK2, CK2alpha), CK2 catalytic subunit alpha

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Val	Val	Val	Ser	Arg	Ser	Gly	Pro	Ser	Thr	Pro	His	Val	Asn	Phe	Leu	465	470	475	480
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Asn	Gln	Asn	Gly	Tyr	Thr	Leu	Val	Ile	Thr	Gly	Lys	Lys	Ile	Thr	Lys	500	505	510	
Ile	Pro	Leu	Asn	Gly	Leu	Gly	Cys	Arg	His	Phe	Gln	Ser	Cys	Ser	Gln	515	520	525	
Cys	Leu	Ser	Ala	Pro	Pro	Phe	Val	Gln	Cys	Gly	Trp	Cys	His	Asp	Lys	530	535	540	
Cys	Val	Arg	Ser	Glu	Glu	Cys	Leu	Ser	Gly	Thr	Trp	Thr	Gln	Gln	Ile	545	550	555	560
Cys	Leu	Pro	Ala	Ile	Tyr	Lys	Val	Phe	Pro	Asn	Ser	Ala	Pro	Leu	Glu	565	570	575	
Gly	Gly	Thr	Arg	Leu	Thr	Ile	Cys	Gly	Trp	Asp	Phe	Gly	Phe	Arg	Arg	580	585	590	
Asn	Asn	Lys	Phe	Asp	Leu	Lys	Lys	Thr	Arg	Val	Leu	Leu	Gly	Asn	Glu	595	600	605	
Ser	Cys	Thr	Leu	Thr	Leu	Ser	Glu	Ser	Thr	Met	Asn	Thr	Leu	Lys	Cys	610	615	620	
Thr	Val	Gly	Pro	Ala	Met	Asn	Lys	His	Phe	Asn	Met	Ser	Ile	Ile	Ile	625	630	635	640
Ser	Asn	Gly	His	Gly	Thr	Thr	Gln	Tyr	Ser	Thr	Phe	Ser	Tyr	Val	Asp	645	650	655	
Pro	Val	Ile	Thr	Ser	Ile	Ser	Pro	Lys	Tyr	Gly	Pro	Met	Ala	Gly	Gly	660	665	670	
Thr	Leu	Leu	Thr	Leu	Thr	Gly	Asn	Tyr	Leu	Asn	Ser	Gly	Asn	Ser	Arg	675	680	685	

His	Ile	Ser	Ile	Gly	Gly	Lys	Thr	Cys	Thr	Leu	Lys	Ser	Val	Ser	Asn	690	695	700
Ser	Ile	Leu	Glu	Cys	Tyr	Thr	Pro	Ala	Gln	Thr	Ile	Ser	Thr	Glu	Phe	705	710	715
Ala	Val	Lys	Leu	Lys	Ile	Asp	Leu	Ala	Asn	Arg	Glu	Thr	Ser	Ile	Phe	725	730	735
Ser	Tyr	Arg	Glu	Asp	Pro	Ile	Val	Tyr	Glu	Ile	His	Pro	Thr	Lys	Ser	740	745	750
Phe	Ile	Ser	Thr	Trp	Trp	Lys	Glu	Pro	Leu	Asn	Ile	Val	Ser	Phe	Leu	755	760	765
Phe	Cys	Phe	Ala	Ser	Gly	Gly	Ser	Thr	Ile	Thr	Gly	Val	Gly	Lys	Asn	770	775	780
Leu	Asn	Ser	Val	Ser	Val	Pro	Arg	Met	Val	Ile	Asn	Val	His	Glu	Ala	785	790	795
Gly	Arg	Asn	Phe	Thr	Val	Ala	Cys	Gln	His	Arg	Ser	Asn	Ser	Glu	Ile	805	810	815
Ile	Cys	Cys	Thr	Thr	Pro	Ser	Leu	Gln	Gln	Leu	Asn	Leu	Gln	Leu	Pro	820	825	830
Leu	Lys	Thr	Lys	Ala	Phe	Phe	Met	Leu	Asp	Gly	Ile	Leu	Ser	Lys	Tyr	835	840	845
Phe	Asp	Leu	Ile	Tyr	Val	His	Asn	Pro	Val	Phe	Lys	Pro	Phe	Glu	Lys	850	855	860
Pro	Val	Met	Ile	Ser	Met	Gly	Asn	Glu	Asn	Val	Leu	Glu	Ile	Lys	Gly	865	870	875
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Thr	Val	Pro	Asn	Asp	Leu	Leu	Lys	Leu	Asn	Ser	Glu	Leu	Asn	Ile	Glu	915	920	925
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Pro	Asp	Gln	Asn	Phe	Thr	Gly	Leu	Ile	Ala	Gly	Val	Val	Ser	Ile	Ser	945	950	955
Thr	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Phe	Phe	Leu	Trp	Leu	Lys	Lys	Arg	965	970	975
Lys	Gln	Ile	Lys	Asp	Leu	Gly	Ser	Glu	Leu	Val	Arg	Tyr	Asp	Ala	Arg	980	985	990
Val	His	Thr	Pro	His	Leu	Asp	Arg	Leu	Val	Ser	Ala	Arg	Ser	Val	Ser	995	1000	1005



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 Gln Val Gln Tyr Pro Leu Thr Asp Met Ser Pro Ile Leu Thr Ser Gly  
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 1075 1080 1085  
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 Lys Lys Ile His Cys Ala Val Lys Ser Leu Asn Arg Ile Thr Asp Ile  
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 Gly Glu Val Ser Gln Phe Leu Thr Glu Gly Ile Ile Met Lys Asp Phe  
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 1155 1160 1165  
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 Lys Phe Thr Val Lys Val Ala Asp Phe Gly Leu Ala Arg Asp Met Tyr  
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 Lys Ser Asp Val Trp Ser Phe Gly Val Val Leu Trp Glu Leu Met Thr  
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<212> DNA

<213> Homo sapiens

<220>

<223> flap structure-specific endonuclease 1 (FEN1)  
 5'-3' exonuclease

<400> 13

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<210> 14

<211> 380

<212> PRT

<213> Homo sapiens

<220>

<223> flap structure-specific endonuclease 1 (FEN1)

5'-3' exonuclease

<400> 14

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```

```

Ala Ile Arg Glu Asn Asp Ile Lys Ser Tyr Phe Gly Arg Lys Val Ala
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```

```

Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln
  35                      40                     45

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```

Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser His Leu
  50                      55                     60

```

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Met Gly Met Phe Tyr Arg Thr Ile Arg Met Met Glu Asn Gly Ile Lys
  65                      70                     75                     80

```

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Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu
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Leu Ala Lys Arg Ser Glu Arg Arg Ala Glu Ala Glu Lys Gln Leu Gln
  100                      105                     110

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Gln Ala Gln Ala Ala Gly Ala Glu Gln Glu Val Glu Lys Phe Thr Lys
  115                      120                     125

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```

Arg Leu Val Lys Val Thr Lys Gln His Asn Asp Glu Cys Lys His Leu
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Leu Ser Leu Met Gly Ile Pro Tyr Leu Asp Ala Pro Ser Glu Ala Glu  
 145 150 155 160  
 Ala Ser Cys Ala Ala Leu Val Lys Ala Gly Lys Val Tyr Ala Ala Ala  
 165 170 175  
 Thr Glu Asp Met Asp Cys Leu Thr Phe Gly Ser Pro Val Leu Met Arg  
 180 185 190  
 His Leu Thr Ala Ser Glu Ala Lys Lys Leu Pro Ile Gln Glu Phe His  
 195 200 205  
 Leu Ser Arg Ile Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val  
 210 215 220  
 Asp Leu Cys Ile Leu Leu Gly Ser Asp Tyr Cys Glu Ser Ile Arg Gly  
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 Ile Gly Pro Lys Arg Ala Val Asp Leu Ile Gln Lys His Lys Ser Ile  
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 Glu Glu Ile Val Arg Arg Leu Asp Pro Asn Lys Tyr Pro Val Pro Glu  
 260 265 270  
 Asn Trp Leu His Lys Glu Ala His Gln Leu Phe Leu Glu Pro Glu Val  
 275 280 285  
 Leu Asp Pro Glu Ser Val Glu Leu Lys Trp Ser Glu Pro Asn Glu Glu  
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 Glu Leu Ile Lys Phe Met Cys Gly Glu Lys Gln Phe Ser Glu Glu Arg  
 305 310 315 320  
 Ile Arg Ser Gly Val Lys Arg Leu Ser Lys Ser Arg Gln Gly Ser Thr  
 325 330 335  
 Gln Gly Arg Leu Asp Asp Phe Phe Lys Val Thr Gly Ser Leu Ser Ser  
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<210> 15

<211> 4276

<212> DNA

<213> Homo sapiens

<220>

<223> REV1 dCMP transferase

<400> 15

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ttacataaat	attaccagag	agcctgatgc	tctctgatag	ctgtgccata	agtgttgtg	4020

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aggatatttgc aaagtgcacg atagtaaatgc tcggagtttt tataatttta aatttcctttt 4080
aaagcaagtgc ttttgtacat ttcttttcaa aaagtgccaa atttgtcagt attgcatgta 4140
aataattgtg ttaattattt tactgtagca tagattctat ttacaaaatg tttgtttata 4200
aagttttatg gattttttaca gtgaagtgtt tacagttgtt taataaagaa ctgtatgtaa 4260
aaaaaaaaaa aaaaaa

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<210> .16
<211> 1251
<212> PRT
<213> Homo sapiens

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<220>
<223> REV1 dCMP transferase

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<400> 16
Met Arg Arg Gly Gly Trp Arg Lys Arg Ala Glu Asn Asp Gly Trp Glu
  1             5             10             15

Thr Trp Gly Gly Tyr Met Ala Ala Lys Val Gln Lys Leu Glu Glu Gln
             20             25             30

Phe Arg Ser Asp Ala Ala Met Gln Lys Asp Gly Thr Ser Ser Thr Ile
             35             40             45

Phe Ser Gly Val Ala Ile Tyr Val Asn Gly Tyr Thr Asp Pro Ser Ala
             50             55             60

Glu Glu Leu Arg Lys Leu Met Met Leu His Gly Gly Gln Tyr His Val
             65             70             75             80

Tyr Tyr Ser Arg Ser Lys Thr Thr His Ile Ile Ala Thr Asn Leu Pro
             85             90             95

Asn Ala Lys Ile Lys Glu Leu Lys Gly Glu Lys Val Ile Arg Pro Glu
             100            105            110

Trp Ile Val Glu Ser Ile Lys Ala Gly Arg Leu Leu Ser Tyr Ile Pro
             115            120            125

Tyr Gln Leu Tyr Thr Lys Gln Ser Ser Val Gln Lys Gly Leu Ser Phe
             130            135            140

Asn Pro Val Cys Arg Pro Glu Asp Pro Leu Pro Gly Pro Ser Asn Ile
             145            150            155            160

Ala Lys Gln Leu Asn Asn Arg Val Asn His Ile Val Lys Lys Ile Glu
             165            170            175

Thr Glu Asn Glu Val Lys Val Asn Gly Met Asn Ser Trp Asn Glu Glu
             180            185            190

Asp Glu Asn Asn Asp Phe Ser Phe Val Asp Leu Glu Gln Thr Ser Pro
             195            200            205

Gly Arg Lys Gln Asn Gly Ile Pro His Pro Arg Gly Ser Thr Ala Ile
             210            215            220

Phe Asn Gly His Thr Pro Ser Ser Asn Gly Ala Leu Lys Thr Gln Asp
             225            230            235            240

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Cys	Leu	Val	Pro	Met	Val	Asn	Ser	Val	Ala	Ser	Arg	Leu	Ser	Pro	Ala	245	250	255
Phe	Ser	Gln	Glu	Glu	Asp	Lys	Ala	Glu	Lys	Ser	Ser	Thr	Asp	Phe	Arg	260	265	270
Asp	Cys	Thr	Leu	Gln	Gln	Leu	Gln	Gln	Ser	Thr	Arg	Asn	Thr	Asp	Ala	275	280	285
Leu	Arg	Asn	Pro	His	Arg	Thr	Asn	Ser	Phe	Ser	Leu	Ser	Pro	Leu	His	290	295	300
Ser	Asn	Thr	Lys	Ile	Asn	Gly	Ala	His	His	Ser	Thr	Val	Gln	Gly	Pro	305	310	315
Ser	Ser	Thr	Lys	Ser	Thr	Ser	Ser	Val	Ser	Thr	Phe	Ser	Lys	Ala	Ala	325	330	335
Pro	Ser	Val	Pro	Ser	Lys	Pro	Ser	Asp	Cys	Asn	Phe	Ile	Ser	Asn	Phe	340	345	350
Tyr	Ser	His	Ser	Arg	Leu	His	His	Ile	Ser	Met	Trp	Lys	Cys	Glu	Leu	355	360	365
Thr	Glu	Phe	Val	Asn	Thr	Leu	Gln	Arg	Gln	Ser	Asn	Gly	Ile	Phe	Pro	370	375	380
Gly	Arg	Glu	Lys	Leu	Lys	Lys	Met	Lys	Thr	Gly	Arg	Ser	Ala	Leu	Val	385	390	395
Val	Thr	Asp	Thr	Gly	Asp	Met	Ser	Val	Leu	Asn	Ser	Pro	Arg	His	Gln	405	410	415
Ser	Cys	Ile	Met	His	Val	Asp	Met	Asp	Cys	Phe	Phe	Val	Ser	Val	Gly	420	425	430
Ile	Arg	Asn	Arg	Pro	Asp	Leu	Lys	Gly	Lys	Pro	Val	Ala	Val	Thr	Ser	435	440	445
Asn	Arg	Gly	Thr	Gly	Arg	Ala	Pro	Leu	Arg	Pro	Gly	Ala	Asn	Pro	Gln	450	455	460
Leu	Glu	Trp	Gln	Tyr	Tyr	Gln	Asn	Lys	Ile	Leu	Lys	Gly	Lys	Ala	Ala	465	470	475
Asp	Ile	Pro	Asp	Ser	Ser	Leu	Trp	Glu	Asn	Pro	Asp	Ser	Ala	Gln	Ala	485	490	495
Asn	Gly	Ile	Asp	Ser	Val	Leu	Ser	Arg	Ala	Glu	Ile	Ala	Ser	Cys	Ser	500	505	510
Tyr	Glu	Ala	Arg	Gln	Leu	Gly	Ile	Lys	Asn	Gly	Met	Phe	Phe	Gly	His	515	520	525
Ala	Lys	Gln	Leu	Cys	Pro	Asn	Leu	Gln	Ala	Val	Pro	Tyr	Asp	Phe	His	530	535	540
Ala	Tyr	Lys	Glu	Val	Ala	Gln	Thr	Leu	Tyr	Glu	Thr	Leu	Ala	Ser	Tyr	545	550	555

Thr His Asn Ile Glu Ala Val Ser Cys Asp Glu Ala Leu Val Asp Ile  
 565 570 575  
 Thr Glu Ile Leu Ala Glu Thr Lys Leu Thr Pro Asp Glu Phe Ala Asn  
 580 585 590  
 Ala Val Arg Met Glu Ile Lys Asp Gln Thr Lys Cys Ala Ala Ser Val  
 595 600 605  
 Gly Ile Gly Ser Asn Ile Leu Leu Ala Arg Met Ala Thr Arg Lys Ala  
 610 615 620  
 Lys Pro Asp Gly Gln Tyr His Leu Lys Pro Glu Glu Val Asp Asp Phe  
 625 630 635 640  
 Ile Arg Gly Gln Leu Val Thr Asn Leu Pro Gly Val Gly His Ser Met  
 645 650 655  
 Glu Ser Lys Leu Ala Ser Leu Gly Ile Lys Thr Cys Gly Asp Leu Gln  
 660 665 670  
 Tyr Met Thr Met Ala Lys Leu Gln Lys Glu Phe Gly Pro Lys Thr Gly  
 675 680 685  
 Gln Met Leu Tyr Arg Phe Cys Arg Gly Leu Asp Asp Arg Pro Val Arg  
 690 695 700  
 Thr Glu Lys Glu Arg Lys Ser Val Ser Ala Glu Ile Asn Tyr Gly Ile  
 705 710 715 720  
 Arg Phe Thr Gln Pro Lys Glu Ala Glu Ala Phe Leu Leu Ser Leu Ser  
 725 730 735  
 Glu Glu Ile Gln Arg Arg Leu Glu Ala Thr Gly Met Lys Gly Lys Arg  
 740 745 750  
 Leu Thr Leu Lys Ile Met Val Arg Lys Pro Gly Ala Pro Val Glu Thr  
 755 760 765  
 Ala Lys Phe Gly Gly His Gly Ile Cys Asp Asn Ile Ala Arg Thr Val  
 770 775 780  
 Thr Leu Asp Gln Ala Thr Asp Asn Ala Lys Ile Ile Gly Lys Ala Met  
 785 790 795 800  
 Leu Asn Met Phe His Thr Met Lys Leu Asn Ile Ser Asp Met Arg Gly  
 805 810 815  
 Val Gly Ile His Val Asn Gln Leu Val Pro Thr Asn Leu Asn Pro Ser  
 820 825 830  
 Thr Cys Pro Ser Arg Pro Ser Val Gln Ser Ser His Phe Pro Ser Gly  
 835 840 845  
 Ser Tyr Ser Val Arg Asp Val Phe Gln Val Gln Lys Ala Lys Lys Ser  
 850 855 860  
 Thr Glu Glu Glu His Lys Glu Val Phe Arg Ala Ala Val Asp Leu Glu  
 865 870 875 880



Ile Ser Ser Ala Ser Arg Thr Cys Thr Phe Leu Pro Pro Phe Pro Ala  
 885 890 895  
 His Leu Pro Thr Ser Pro Asp Thr Asn Lys Ala Glu Ser Ser Gly Lys  
 900 905 910  
 Trp Asn Gly Leu His Thr Pro Val Ser Val Gln Ser Arg Leu Asn Leu  
 915 920 925  
 Ser Ile Glu Val Pro Ser Pro Ser Gln Leu Asp Gln Ser Val Leu Glu  
 930 935 940  
 Ala Leu Pro Pro Asp Leu Arg Glu Gln Val Glu Gln Val Cys Ala Val  
 945 950 955 960  
 Gln Gln Ala Glu Ser His Gly Asp Lys Lys Lys Glu Pro Val Asn Gly  
 965 970 975  
 Cys Asn Thr Gly Ile Leu Pro Gln Pro Val Gly Thr Val Leu Leu Gln  
 980 985 990  
 Ile Pro Glu Pro Gln Glu Ser Asn Ser Asp Ala Gly Ile Asn Leu Ile  
 995 1000 1005  
 Ala Leu Pro Ala Phe Ser Gln Val Asp Pro Glu Val Phe Ala Ala Leu  
 1010 1015 1020  
 Pro Ala Glu Leu Gln Arg Glu Leu Lys Ala Ala Tyr Asp Gln Arg Gln  
 1025 1030 1035 1040  
 Arg Gln Gly Glu Asn Ser Thr His Gln Gln Ser Ala Ser Ala Ser Val  
 1045 1050 1055  
 Pro Lys Asn Pro Leu Leu His Leu Lys Ala Ala Val Lys Glu Lys Lys  
 1060 1065 1070  
 Arg Asn Lys Lys Lys Lys Thr Ile Gly Ser Pro Lys Arg Ile Gln Ser  
 1075 1080 1085  
 Pro Leu Asn Asn Lys Leu Leu Asn Ser Pro Ala Lys Thr Leu Pro Gly  
 1090 1095 1100  
 Ala Cys Gly Ser Pro Gln Lys Leu Ile Asp Gly Phe Leu Lys His Glu  
 1105 1110 1115 1120  
 Gly Pro Pro Ala Glu Lys Pro Leu Glu Glu Leu Ser Ala Ser Thr Ser  
 1125 1130 1135  
 Gly Val Pro Gly Leu Ser Ser Leu Gln Ser Asp Pro Ala Gly Cys Val  
 1140 1145 1150  
 Arg Pro Pro Ala Pro Asn Leu Ala Gly Ala Val Glu Phe Asn Asp Val  
 1155 1160 1165  
 Lys Thr Leu Leu Arg Glu Trp Ile Thr Thr Ile Ser Asp Pro Met Glu  
 1170 1175 1180  
 Glu Asp Ile Leu Gln Val Val Lys Tyr Cys Thr Asp Leu Ile Glu Glu  
 1185 1190 1195 1200

Lys Asp Leu Glu Lys Leu Asp Leu Val Ile Lys Tyr Met Lys Arg Leu  
 1205 1210 1215  
 Met Gln Gln Ser Val Glu Ser Val Trp Asn Met Ala Phe Asp Phe Ile  
 1220 1225 1230  
 Leu Asp Asn Val Gln Val Val Leu Gln Gln Thr Tyr Gly Ser Thr Leu  
 1235 1240 1245  
 Lys Val Thr  
 1250

<210> 17  
 <211> 2957  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> apyrimidinic endonuclease 1 (APE1), AP  
 endonuclease 1, HAP1

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 ctccagggac ctgtcttcct aacgtccagg gagccccgag caactcgcgc cttacattcg 120  
 tatccgtttt cctatctctt tcccgtgggt agcccagcct tctccactgt ttttttcctc 180  
 ttgcacagag ttagaatctt aagtcagtgt cacacaatgt gctgtgcatc tggcacaacg 240  
 ataaacagcc gagggagggg tggggactaa gtgcctagag aattagagga gggaggcgag 300  
 gctaagcgtc cgtcacgtgg tgtcagacag accaatcacg cgcattcttc ggccacgaca 360  
 agcgcgcctc tgatcacgtg accaggtccg ctaccacagt gggggctcag cgtgcacctc 420  
 tctttgtgct cgggttagga ggagctaggg tgccatcggg ccggtgcaga tacgggggtg 480  
 ctcttttgct cataagaggg gcttcgctgg cagtctgaac ggcaagcttg agtcaggacc 540  
 cttaattaag atcctcaatt ggctggaggg cagatctcgc gagtagggta caaggcacta 600  
 tgaaatgata tagtttcgtg ggtgaggggc tgaagggcct atgatgcacg gaggcgggga 660  
 aaggatttag agataacgtg gtttaaaggc gggacctggg gcggggacgc tccttgggag 720  
 gagtcttctc ccagccttag ctggtttcat gatttctttg cgtctgtagg caacgcggta 780  
 aaaatattgc ttcggtgggt gacgcggtac agctgccccaa gggcgttcgt aacgggaatg 840  
 ccgaagcgtg ggaaaaaggg agcgggtggcg gaagacgggg atgagctcag gacaggtaaag 900  
 ggaatgaaat cagcccttct tccatagaagc tgcggcgggg gtgtttgtca ttcccttgat 960  
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 taggctttcg ttgggtctat agttaacgcc ggatcgagc tggaaaaccac cagctttttg 1080  
 tcagtatata ttactcattt tatagagcca gagggcaaga agagtaagac ggccgcaaag 1140  
 aaaaatgaca aagaggcagc aggagagggc ccagccctgt atgaggaccc cccagatcag 1200  
 aaaacctcac ccagtggcaa acctgccaca ctcaagatct gctcttgga tgtggatggg 1260  
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 ctgttttatt tttctcctgc ccgtagtttt ctgtggggct tccccagctc tgccagttgt 1440  
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 cttcccagaa tgttgcaaaa acctcttcac tatacttcc ccatcttatc ttccctgcatt 1560  
 gcattccata tgaagcatgt cctccattcc attaaccata gcttaaaatc ttagcttgct 1620  
 atccactgcc tatagaaaaa acacatctcc ttggcatagc atgtaagact ttcttacctc 1680  
 tctatatattg ttttcattta tctagcttag aattgtttga atattgtgct gcttgactcg 1740  
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 ttcaataaat gttctgctga attgataata cgttttccac ctttcttttc acttacagtg 1860  
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 ggacaaggaa ggttacagtg gcgtgggcct gctttccgcg cagtgccac tcaaagtttc 2040  
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 aattctctat ctctgcccc cctcttgatt gctttccctt ttcttatagt tttttatgct 2160  
 aattctgttt catttctata ggcatgagg agcatgatca ggaaggccgg gtgattgtgg 2220  
 ctgaatttga ctcgtttgtg ctggtaacag catatgtacc taatgcaggc cgaggtctgg 2280

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tacgactgga gtaccggcag cgctgggatg aagcctttcg caagttcctg aagggcctgg 2340
cttcccgaaa gcccttgtg ctgtgtggag acctcaatgt ggcacatgaa gaaattgacc 2400
ttcgcaaccc caaggggaac aaaaagaatg ctggcttcac gccacaagag cgccaaggct 2460
tcgggggaatt actgcaggct gtgccactgg ctgacagctt taggcacctc taccccaaca 2520
caccctatgc ctacaccttt tggacttata tgatgaatgc tcgatccaag aatgttggtt 2580
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aaacactctt cagagaaatc tgcattctat ttctcatgta taaaactagg aatcctccaa 2820
ccaggctcct gtgatagagt tcttttaagc ccaagatttt ttatttgagg gttttttgtt 2880
ttttaaaaaa aaattgaaca aagactacta atgactttgt ttgaattatc cacatgaaaa 2940
taaagagcca tagtttc 2957

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<210> 18
<211> 318
<212> PRT
<213> Homo sapiens

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<220>
<223> apyrimidinic endonuclease 1 (APE1), AP
      endonuclease 1, HAP1

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<400> 18
Met Pro Lys Arg Gly Lys Lys Gly Ala Val Ala Glu Asp Gly Asp Glu
  1             5             10             15

Leu Arg Thr Glu Pro Glu Ala Lys Lys Ser Lys Thr Ala Ala Lys Lys
      20             25             30

Asn Asp Lys Glu Ala Ala Gly Glu Gly Pro Ala Leu Tyr Glu Asp Pro
      35             40             45

Pro Asp Gln Lys Thr Ser Pro Ser Gly Lys Pro Ala Thr Leu Lys Ile
      50             55             60

Cys Ser Trp Asn Val Asp Gly Leu Arg Ala Trp Ile Lys Lys Lys Gly
      65             70             75             80

Leu Asp Trp Val Lys Glu Glu Ala Pro Asp Ile Leu Cys Leu Gln Glu
      85             90             95

Thr Lys Cys Ser Glu Asn Lys Leu Pro Ala Glu Leu Gln Glu Leu Pro
      100            105            110

Gly Leu Ser His Gln Tyr Trp Ser Ala Pro Ser Asp Lys Glu Gly Tyr
      115            120            125

Ser Gly Val Gly Leu Leu Ser Arg Gln Cys Pro Leu Lys Val Ser Tyr
      130            135            140

Gly Ile Gly Asp Glu Glu His Asp Gln Glu Gly Arg Val Ile Val Ala
      145            150            155            160

Glu Phe Asp Ser Phe Val Leu Val Thr Ala Tyr Val Pro Asn Ala Gly
      165            170            175

Arg Gly Leu Val Arg Leu Glu Tyr Arg Gln Arg Trp Asp Glu Ala Phe
      180            185            190

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Arg Lys Phe Leu Lys Gly Leu Ala Ser Arg Lys Pro Leu Val Leu Cys  
 195 200 205  
 Gly Asp Leu Asn Val Ala His Glu Glu Ile Asp Leu Arg Asn Pro Lys  
 210 215 220  
 Gly Asn Lys Lys Asn Ala Gly Phe Thr Pro Gln Glu Ala Gln Gly Phe  
 225 230 235 240  
 Gly Glu Leu Leu Gln Ala Val Pro Leu Ala Asp Ser Phe Arg His Leu  
 245 250 255  
 Tyr Pro Asn Thr Pro Tyr Ala Tyr Thr Phe Trp Thr Tyr Met Met Asn  
 260 265 270  
 Ala Arg Ser Lys Asn Val Gly Trp Arg Leu Asp Tyr Phe Leu Leu Ser  
 275 280 285  
 His Ser Leu Leu Pro Ala Leu Cys Asp Ser Lys Ile Arg Ser Lys Ala  
 290 295 300  
 Leu Gly Ser Asp His Cys Pro Ile Thr Leu Tyr Leu Ala Leu  
 305 310 315

<210> 19

<211> 1161

<212> DNA

<213> Homo sapiens

<220>

<223> cyclin-dependent kinase 3 (CDK3), cyclin-dependent protein kinase

<400> 19

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ccacatggaa gctggaggag caaccgggag cgctgggctg gggtgcaa at tgcccagtg 60
cttctgtttc ccaggcagct ctgtggccat ggatatgttc cagaaggtag agaagatcgg 120
agagggcacc tatgggggtg tgtacaaggc caagaacagg gagacagggc agctggtggc 180
cctgaagaag atcagactgg atttgagat ggaggggggtc ccaagcactg ccatcagggg 240
gatctcgctg ctcaaggaac tgaagcacc caacatcgtc cgactgctgg acgtggtgca 300
caacgagagg aagctctatc tgggtgtttga gttcctcagc caggacctga agaagtacat 360
ggactccacc ccaggctcag agctccccct gcacctcatc aagagctacc tcttccagct 420
gctgcagggg gtgagtttct gccactcaca tggggtcatc caccgagacc tgaagcccca 480
gaacctgctc atcaatgagt tgggtgccat caagctggct gacttcggcc tggctcgcg 540
cttcgggggtg cccctgcgca cctacaccca tgaggtggtg acactgtggt atcgcgcccc 600
cgagattctc ttgggcagca agttctatac cacagctgtg gatattctgga gcattggttg 660
catctttgca gagatggtga ctcgaaaagc cctgtttcct ggtgactctg agattgacca 720
gctctttcgt atctttcgta tgctggggac accagcgaa gacacatggc ccgggggtcac 780
ccagctgcct gactataagg gcagcttccc taagtggacc aggaagggac tgggaagagat 840
tgtgccc aat ctggagccag agggcagggg cctgctcatg caactcctgc agtatgacct 900
cagccagcgg atcacagcca agactgcctt ggccaccccg tacttctcat cccctgagcc 960
ctcccagct gcccgccagt atgtgctgca gcgattccgc cattgagaat gtcaaggcca 1020
cactcagatc ctttctcgag cagcagctgc tgcccagct gcctcctacc cattgccaa 1080
agaggatgca tctggggaga gcaaagcact aaggaattca gcatcagcct gcagagggt 1140
gagtctgggt tagtctctgcc c 1161
  
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<210> 20

<211> 305

<212> PRT

<213> Homo sapiens

<220>

<223> cyclin-dependent kinase 3 (CDK3), cyclin-dependent  
protein kinase

<400> 20

Met	Asp	Met	Phe	Gln	Lys	Val	Glu	Lys	Ile	Gly	Glu	Gly	Thr	Tyr	Gly	
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Val	Val	Tyr	Lys	Ala	Lys	Asn	Arg	Glu	Thr	Gly	Gln	Leu	Val	Ala	Leu	
			20					25					30			
Lys	Lys	Ile	Arg	Leu	Asp	Leu	Glu	Met	Glu	Gly	Val	Pro	Ser	Thr	Ala	
		35					40					45				
Ile	Arg	Glu	Ile	Ser	Leu	Leu	Lys	Glu	Leu	Lys	His	Pro	Asn	Ile	Val	
	50					55					60					
Arg	Leu	Leu	Asp	Val	Val	His	Asn	Glu	Arg	Lys	Leu	Tyr	Leu	Val	Phe	
65					70					75					80	
Glu	Phe	Leu	Ser	Gln	Asp	Leu	Lys	Lys	Tyr	Met	Asp	Ser	Thr	Pro	Gly	
				85					90					95		
Ser	Glu	Leu	Pro	Leu	His	Leu	Ile	Lys	Ser	Tyr	Leu	Phe	Gln	Leu	Leu	
			100					105					110			
Gln	Gly	Val	Ser	Phe	Cys	His	Ser	His	Arg	Val	Ile	His	Arg	Asp	Leu	
		115					120					125				
Lys	Pro	Gln	Asn	Leu	Leu	Ile	Asn	Glu	Leu	Gly	Ala	Ile	Lys	Leu	Ala	
	130					135					140					
Asp	Phe	Gly	Leu	Ala	Arg	Ala	Phe	Gly	Val	Pro	Leu	Arg	Thr	Tyr	Thr	
145					150					155					160	
His	Glu	Val	Val	Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Leu	Leu	Gly	
				165					170					175		
Ser	Lys	Phe	Tyr	Thr	Thr	Ala	Val	Asp	Ile	Trp	Ser	Ile	Gly	Cys	Ile	
			180					185					190			
Phe	Ala	Glu	Met	Val	Thr	Arg	Lys	Ala	Leu	Phe	Pro	Gly	Asp	Ser	Glu	
		195					200					205				
Ile	Asp	Gln	Leu	Phe	Arg	Ile	Phe	Arg	Met	Leu	Gly	Thr	Pro	Ser	Glu	
	210					215					220					
Asp	Thr	Trp	Pro	Gly	Val	Thr	Gln	Leu	Pro	Asp	Tyr	Lys	Gly	Ser	Phe	
225					230					235					240	
Pro	Lys	Trp	Thr	Arg	Lys	Gly	Leu	Glu	Glu	Ile	Val	Pro	Asn	Leu	Glu	
				245				250						255		
Pro	Glu	Gly	Arg	Asp	Leu	Leu	Met	Gln	Leu	Leu	Gln	Tyr	Asp	Pro	Ser	
			260					265					270			
Gln	Arg	Ile	Thr	Ala	Lys	Thr	Ala	Leu	Ala	His	Pro	Tyr	Phe	Ser	Ser	
		275					280						285			

Pro Glu Pro Ser Pro Ala Ala Arg Gln Tyr Val Leu Gln Arg Phe Arg  
 290 295 300

His  
 305

<210> 21  
 <211> 2297  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> PIM1 oncogene serine threonine kinase

<400> 21  
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 cgccccgcgcc tgcaacgacc tgcacgccac caagctggcg ccgggcaagg agaaggagcc 120  
 cctggaggtcg cagtaccagg tggggcccgt actgggcagc ggcggttcg gctcgggtcta 180  
 ctcaggcgtc cgcgctctccg acaacttgcc ggtggccatc aaacacgtgg agaaggaccg 240  
 gatttccgac tggggagagc tgcctaattg cactcgagtg cccatggaag tggtcctgct 300  
 gaagaagggtg agctcggggt tctccggcgt cattaggctc ctggactggt tcgagaggcc 360  
 cgacagtttc gtcctgatcc tggagaggcc cgagccggtg caagatctct tcgacttcat 420  
 cacggaaaagg ggagccctgc aagaggagct ggccccgagc ttcttctggc aggtgctgga 480  
 ggccgtgctg cactgccaca actgcggggt gctccaccgc gacatcaagg acgaaaacat 540  
 ccttatcgac ctcaatcgcg gcgagctcaa gctcatcgac ttcgggtcgg gggcgctgct 600  
 caaggacacc gtctacacgg acttcgatgg gacccgagtg tatagccctc cagagtggat 660  
 ccgctaccat cgctaccatg gcaggtcggc ggcagttctg tccctgggga tcctgctgta 720  
 tgatattggtg tgtggagata ttcttttcga gcattgacgaa gagatcatca ggggccaggt 780  
 tttcttcagg cagagggtct cttcagaatg tcagcatctc attagatggt gcttggccct 840  
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<210> 22  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

<220>

<223> PIM1 oncogene serine threonine kinase

<400> 22

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      20             25             30

Pro Leu Glu Ser Gln Tyr Gln Val Gly Pro Leu Leu Gly Ser Gly Gly
      35             40             45

Phe Gly Ser Val Tyr Ser Gly Ile Arg Val Ser Asp Asn Leu Pro Val
      50             55             60

Ala Ile Lys His Val Glu Lys Asp Arg Ile Ser Asp Trp Gly Glu Leu
      65             70             75             80

Pro Asn Gly Thr Arg Val Pro Met Glu Val Val Leu Leu Lys Lys Val
      85             90             95

Ser Ser Gly Phe Ser Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg
      100            105            110

Pro Asp Ser Phe Val Leu Ile Leu Glu Arg Pro Glu Pro Val Gln Asp
      115            120            125

Leu Phe Asp Phe Ile Thr Glu Arg Gly Ala Leu Gln Glu Glu Leu Ala
      130            135            140

Arg Ser Phe Phe Trp Gln Val Leu Glu Ala Val Arg His Cys His Asn
      145            150            155            160

Cys Gly Val Leu His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp
      165            170            175

Leu Asn Arg Gly Glu Leu Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu
      180            185            190

Leu Lys Asp Thr Val Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser
      195            200            205

Pro Pro Glu Trp Ile Arg Tyr His Arg Tyr His Gly Arg Ser Ala Ala
      210            215            220

Val Trp Ser Leu Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile
      225            230            235            240

Pro Phe Glu His Asp Glu Glu Ile Ile Arg Gly Gln Val Phe Phe Arg
      245            250            255

Gln Arg Val Ser Ser Glu Cys Gln His Leu Ile Arg Trp Cys Leu Ala
      260            265            270

Leu Arg Pro Ser Asp Arg Pro Thr Phe Glu Glu Ile Gln Asn His Pro
      275            280            285
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His Ser Leu Ser Pro Gly Pro Ser Lys  
 305 310

<210> 23  
 <211> 3178  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> CDC7 cell division cycle 7 (CDC7), CDC7 cell  
 division cycle 7-like 1 (CDC7L1) protein serine  
 threonine kinase

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<210> 24
<211> 574
<212> PRT
<213> Homo sapiens

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<220>
<223> CDC7 cell division cycle 7 (CDC7), CDC7 cell
      division cycle 7-like 1 (CDC7L1) protein serine
      threonine kinase

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<400> 24
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Pro Gln Arg Asp Arg Phe Gln Ala Glu Gly Ser Leu Lys Lys Asn Glu
      20             25             30

Gln Asn Phe Lys Leu Ala Gly Val Lys Lys Asp Ile Glu Lys Leu Tyr
      35             40             45

Glu Ala Val Pro Gln Leu Ser Asn Val Phe Lys Ile Glu Asp Lys Ile
      50             55             60

Gly Glu Gly Thr Phe Ser Ser Val Tyr Leu Ala Thr Ala Gln Leu Gln
      65             70             75             80

Val Gly Pro Glu Glu Lys Ile Ala Leu Lys His Leu Ile Pro Thr Ser
      85             90             95

His Pro Ile Arg Ile Ala Ala Glu Leu Gln Cys Leu Thr Val Ala Gly
      100            105            110

Gly Gln Asp Asn Val Met Gly Val Lys Tyr Cys Phe Arg Lys Asn Asp
      115            120            125

His Val Val Ile Ala Met Pro Tyr Leu Glu His Glu Ser Phe Leu Asp
      130            135            140

Ile Leu Asn Ser Leu Ser Phe Gln Glu Val Arg Glu Tyr Met Leu Asn
      145            150            155            160

Leu Phe Lys Ala Leu Lys Arg Ile His Gln Phe Gly Ile Val His Arg
      165            170            175

Asp Val Lys Pro Ser Asn Phe Leu Tyr Asn Arg Arg Leu Lys Lys Tyr
      180            185            190

Ala Leu Val Asp Phe Gly Leu Ala Gln Gly Thr His Asp Thr Lys Ile
      195            200            205

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Glu Leu Leu Lys Phe Val Gln Ser Glu Ala Gln Gln Glu Arg Cys Ser  
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 Pro Val Pro Lys Glu Leu Asp Gln Gln Ser Thr Thr Lys Ala Ser Val  
 245 250 255  
 Lys Arg Pro Tyr Thr Asn Ala Gln Ile Gln Ile Lys Gln Gly Lys Asp  
 260 265 270  
 Gly Lys Glu Gly Ser Val Gly Leu Ser Val Gln Arg Ser Val Phe Gly  
 275 280 285  
 Glu Arg Asn Phe Asn Ile His Ser Ser Ile Ser His Glu Ser Pro Ala  
 290 295 300  
 Val Lys Leu Met Lys Gln Ser Lys Thr Val Asp Val Leu Ser Arg Lys  
 305 310 315 320  
 Leu Ala Thr Lys Lys Lys Ala Ile Ser Thr Lys Val Met Asn Ser Ala  
 325 330 335  
 Val Met Arg Lys Thr Ala Ser Ser Cys Pro Ala Ser Leu Thr Cys Asp  
 340 345 350  
 Cys Tyr Ala Thr Asp Lys Val Cys Ser Ile Cys Leu Ser Arg Arg Gln  
 355 360 365  
 Gln Val Ala Pro Arg Ala Gly Thr Pro Gly Phe Arg Ala Pro Glu Val  
 370 375 380  
 Leu Thr Lys Cys Pro Asn Gln Thr Thr Ala Ile Asp Met Trp Ser Ala  
 385 390 395 400  
 Gly Val Ile Phe Leu Ser Leu Leu Ser Gly Arg Tyr Pro Phe Tyr Lys  
 405 410 415  
 Ala Ser Asp Asp Leu Thr Ala Leu Ala Gln Ile Met Thr Ile Arg Gly  
 420 425 430  
 Ser Arg Glu Thr Ile Gln Ala Ala Lys Thr Phe Gly Lys Ser Ile Leu  
 435 440 445  
 Cys Ser Lys Glu Val Pro Ala Gln Asp Leu Arg Lys Leu Cys Glu Arg  
 450 455 460  
 Leu Arg Gly Met Asp Ser Ser Thr Pro Lys Leu Thr Ser Asp Ile Gln  
 465 470 475 480  
 Gly His Ala Ser His Gln Pro Ala Ile Ser Glu Lys Thr Asp His Lys  
 485 490 495  
 Ala Ser Cys Leu Val Gln Thr Pro Pro Gly Gln Tyr Ser Gly Asn Ser  
 500 505 510  
 Phe Lys Lys Gly Asp Ser Asn Ser Cys Glu His Cys Phe Asp Glu Tyr  
 515 520 525

Asn Thr Asn Leu Glu Gly Trp Asn Glu Val Pro Asp Glu Ala Tyr Asp  
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Leu Leu Asp Lys Leu Leu Asp Leu Asn Pro Ala Ser Arg Ile Thr Ala  
 545 550 555 560

Glu Glu Ala Leu Leu His Pro Phe Phe Lys Asp Met Ser Leu  
 565 570

<210> 25

<211> 1427

<212> DNA

<213> Homo sapiens

<220>

<223> cyclin-dependent kinase 7 (CDK7), kinase subunit  
 of Cdk-activating kinase (CAK), kinase component  
 of transcription factor complex TFIIH

<400> 25

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<210> 26

<211> 346

<212> PRT

<213> Homo sapiens

<220>

<223> cyclin-dependent kinase 7 (CDK7), kinase subunit  
 of Cdk-activating kinase (CAK), kinase component  
 of transcription factor complex TFIIH

<400> 26

Met Ala Leu Asp Val Lys Ser Arg Ala Lys Arg Tyr Glu Lys Leu Asp  
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Asn	Thr	Asn	Gln	Ile	Val	Ala	Ile	Lys	Lys	Ile	Lys	Leu	Gly	His	Arg	35	40	45	
Ser	Glu	Ala	Lys	Asp	Gly	Ile	Asn	Arg	Thr	Ala	Leu	Arg	Glu	Ile	Lys	50	55	60	
Leu	Leu	Gln	Glu	Leu	Ser	His	Pro	Asn	Ile	Ile	Gly	Leu	Leu	Asp	Ala	65	70	75	80
Phe	Gly	His	Lys	Ser	Asn	Ile	Ser	Leu	Val	Phe	Asp	Phe	Met	Glu	Thr	85	90	95	
Asp	Leu	Glu	Val	Ile	Ile	Lys	Asp	Asn	Ser	Leu	Val	Leu	Thr	Pro	Ser	100	105	110	
His	Ile	Lys	Ala	Tyr	Met	Leu	Met	Thr	Leu	Gln	Gly	Leu	Glu	Tyr	Leu	115	120	125	
His	Gln	His	Trp	Ile	Leu	His	Arg	Asp	Leu	Lys	Pro	Asn	Asn	Leu	Leu	130	135	140	
Leu	Asp	Glu	Asn	Gly	Val	Leu	Lys	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Lys	145	150	155	160
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Arg	Val	Pro	Phe	Leu	Pro	Gly	Asp	Ser	Asp	Leu	Asp	Gln	Leu	Thr	Arg	210	215	220	
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Cys	Ser	Leu	Pro	Asp	Tyr	Val	Thr	Phe	Lys	Ser	Phe	Pro	Gly	Ile	Pro	245	250	255	
Leu	His	His	Ile	Phe	Ser	Ala	Ala	Gly	Asp	Asp	Leu	Leu	Asp	Leu	Ile	260	265	270	
Gln	Gly	Leu	Phe	Leu	Phe	Asn	Pro	Cys	Ala	Arg	Ile	Thr	Ala	Thr	Gln	275	280	285	
Ala	Leu	Lys	Met	Lys	Tyr	Phe	Ser	Asn	Arg	Pro	Gly	Pro	Thr	Pro	Gly	290	295	300	
Cys	Gln	Leu	Pro	Arg	Pro	Asn	Cys	Pro	Val	Glu	Thr	Leu	Lys	Glu	Gln	305	310	315	320

Ser Asn Pro Ala Leu Ala Ile Lys Arg Lys Arg Thr Glu Ala Leu Glu  
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Gln Gly Gly Leu Pro Lys Lys Leu Ile Phe  
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<210> 27  
<211> 2169  
<212> DNA  
<213> Homo sapiens

<220>  
<223> cytokine-inducible kinase (CNK) serine threonine  
kinase, proliferation-related kinase (PRK),  
polo-like kinase 3 (PLK3)

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<210> 28  
<211> 607  
<212> PRT  
<213> Homo sapiens

<220>

<223> cytokine-inducible kinase (CNK) serine threonine  
kinase, proliferation-related kinase (PRK),  
polo-like kinase 3 (PLK3)

<400> 28

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Gly	Phe	Ala	Arg	Cys	Tyr	Glu	Ala	Thr	Asp	Thr	Glu	Thr	Gly	Ser	Ala	
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Tyr	Ala	Val	Lys	Val	Ile	Pro	Gln	Ser	Arg	Val	Ala	Lys	Pro	His	Gln	
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Arg	Glu	Lys	Ile	Leu	Asn	Glu	Ile	Glu	Leu	His	Arg	Asp	Leu	Gln	His	
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Arg	His	Ile	Val	Arg	Phe	Ser	His	His	Phe	Glu	Asp	Ala	Asp	Asn	Ile	
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Tyr	Ile	Phe	Leu	Glu	Leu	Cys	Ser	Arg	Lys	Ser	Leu	Ala	His	Ile	Trp	
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Lys	Ala	Arg	His	Thr	Leu	Leu	Glu	Pro	Glu	Val	Arg	Tyr	Tyr	Leu	Arg	
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Gln	Ile	Leu	Ser	Gly	Leu	Lys	Tyr	Leu	His	Gln	Arg	Gly	Ile	Leu	His	
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Arg	Lys	Lys	Thr	Ile	Cys	Gly	Thr	Pro	Asn	Tyr	Val	Ala	Pro	Glu	Val	
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Leu	Leu	Arg	Gln	Gly	His	Gly	Pro	Glu	Ala	Asp	Val	Trp	Ser	Leu	Gly	
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Arg	Ala	Ser	Pro	Arg	Asp	Arg	Pro	Ser	Ile	Asp	Gln	Ile	Leu	Arg	His	
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		275					280					285				

Cys	Val	Thr	Val	Pro	Asp	Leu	Thr	Pro	Pro	Asn	Pro	Ala	Arg	Ser	Leu	290	295	300
Phe	Ala	Lys	Val	Thr	Lys	Ser	Leu	Phe	Gly	Arg	Lys	Lys	Lys	Ser	Lys	305	310	315
Asn	His	Ala	Gln	Glu	Arg	Asp	Glu	Val	Ser	Gly	Leu	Val	Ser	Gly	Leu	325	330	335
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Ser	Ser	Pro	Arg	Gly	Thr	Leu	Ala	Ser	Ser	Gly	Asp	Gly	Phe	Glu	Glu	370	375	380
Gly	Leu	Thr	Val	Ala	Thr	Val	Val	Glu	Ser	Ala	Leu	Cys	Ala	Leu	Arg	385	390	395
Asn	Cys	Ile	Ala	Phe	Met	Pro	Pro	Ala	Glu	Gln	Asn	Pro	Ala	Pro	Leu	405	410	415
Ala	Gln	Pro	Glu	Pro	Leu	Val	Trp	Val	Ser	Lys	Trp	Val	Asp	Tyr	Ser	420	425	430
Asn	Lys	Phe	Gly	Phe	Gly	Tyr	Gln	Leu	Ser	Ser	Arg	Arg	Val	Ala	Val	435	440	445
Leu	Phe	Asn	Asp	Gly	Thr	His	Met	Ala	Leu	Ser	Ala	Asn	Arg	Lys	Thr	450	455	460
Val	His	Tyr	Asn	Pro	Thr	Ser	Thr	Lys	His	Phe	Ser	Phe	Ser	Val	Gly	465	470	475
Ala	Val	Pro	Arg	Ala	Leu	Gln	Pro	Gln	Leu	Gly	Ile	Leu	Arg	Tyr	Phe	485	490	495
Ala	Ser	Tyr	Met	Glu	Gln	His	Leu	Met	Lys	Gly	Gly	Asp	Leu	Pro	Ser	500	505	510
Val	Glu	Glu	Val	Glu	Val	Pro	Ala	Pro	Pro	Leu	Leu	Leu	Gln	Trp	Val	515	520	525
Lys	Thr	Asp	Gln	Ala	Leu	Leu	Met	Leu	Phe	Ser	Asp	Gly	Thr	Val	Gln	530	535	540
Val	Asn	Phe	Tyr	Gly	Asp	His	Thr	Lys	Leu	Ile	Leu	Ser	Gly	Trp	Glu	545	550	555
Pro	Leu	Leu	Val	Thr	Phe	Val	Ala	Arg	Asn	Arg	Ser	Ala	Cys	Thr	Tyr	565	570	575
Leu	Ala	Ser	His	Leu	Arg	Gln	Leu	Gly	Cys	Ser	Pro	Asp	Leu	Arg	Gln	580	585	590
Arg	Leu	Arg	Tyr	Ala	Leu	Arg	Leu	Leu	Arg	Asp	Arg	Ser	Pro	Ala		595	600	605

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 <211> 1321  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> potentially prenylated protein tyrosine  
 phosphatase (PRL-3), protein tyrosine phosphatase  
 type IVA, member 3, isoform 2, transcript variant  
 2 (PTP4A3)

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 phosphatase (PRL-3), protein tyrosine phosphatase  
 type IVA, member 3, isoform 2, transcript variant  
 2 (PTP4A3)

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 Cys Glu Val Thr Tyr Asp Lys Thr Pro Leu Glu Lys Asp Gly Ile Thr  
 50 55 60



Val Val Asp Trp Pro Phe Asp Asp Gly Ala Pro Pro Pro Gly Lys Val  
65 70 75 80

Val Glu Asp Trp Leu Ser Leu Val Lys Ala Lys Phe Cys Glu Ala Pro  
85 90 95

Gly Ser Cys Val Ala Val His Cys Val Ala Gly Leu Gly Arg Lys Arg  
100 105 110

Arg Gly Ala Ile Asn Ser Lys Gln Leu Thr Tyr Leu Glu Lys Tyr Arg  
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Cys Cys Val Met  
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<211> 3696

<212> DNA

<213> Homo sapiens

<220>

<223> serine threonine kinase 2 (STK2, NEK4)

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<210> 32

<211> 841

<212> PRT

<213> Homo sapiens

<220>

<223> serine threonine kinase 2 (STK2, NEK4)

<400> 32

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Val Ile Lys Lys Leu Asn Leu Arg Asn Ala Ser Ser Arg Glu Arg Arg
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Ile Val Thr Tyr Lys Glu Ser Trp Glu Gly Gly Asp Gly Leu Leu Tyr
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Ile Val Met Gly Phe Cys Glu Gly Gly Asp Leu Tyr Arg Lys Leu Lys
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Glu Gln Lys Gly Gln Leu Leu Pro Glu Asn Gln Val Val Glu Trp Phe
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Ile	Lys	Val	Gly	Asp	Leu	Gly	Ile	Ala	Arg	Val	Leu	Glu	Asn	His	Cys	145	150	155
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Leu	Phe	Ser	Asn	Lys	Pro	Tyr	Asn	Tyr	Lys	Ser	Asp	Val	Trp	Ala	Leu	180	185	190
Gly	Cys	Cys	Val	Tyr	Glu	Met	Ala	Thr	Leu	Lys	His	Ala	Phe	Asn	Ala	195	200	205
Lys	Asp	Met	Asn	Ser	Leu	Val	Tyr	Arg	Ile	Ile	Glu	Gly	Lys	Leu	Pro	210	215	220
Pro	Met	Pro	Arg	Asp	Tyr	Ser	Pro	Glu	Leu	Ala	Glu	Leu	Ile	Arg	Thr	225	230	235
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Lys	Glu	Ser	Cys	Glu	Asp	Val	Pro	Val	Ala	Asn	Pro	Val	Ser	Glu	Phe	725	730	735	
Lys	Leu	His	Arg	Lys	Tyr	Arg	Asp	Thr	Leu	Ile	Leu	His	Gly	Lys	Val	740	745	750	

Ala Glu Glu Ala Glu Glu Ile His Phe Lys Glu Leu Pro Ser Ala Ile  
755 760 765

Met Pro Gly Ser Glu Lys Ile Arg Arg Leu Val Glu Val Leu Arg Thr  
770 775 780

Asp Val Ile Arg Gly Leu Gly Val Gln Leu Leu Glu Gln Val Tyr Asp  
785 790 795 800

Leu Leu Glu Glu Glu Asp Glu Phe Asp Arg Glu Val Arg Leu Arg Glu  
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<210> 33  
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kinase-related protein kinase NKIATRE homologue

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cctgtggata tctgggcttt gggctgtatg atcattgaga tggccactgg aaatccctat 600  
cttcttagta gttctgattt ggatttactc cataaaattg ttttgaaagt gggcaatttg 660  
tcacctcact tgcagaatat cttttccaag agccccattt ttgctggggg agttcttcct 720  
caagttcaac accccaaaaa tgcaagaaaa aaatatccaa agcttaatgg attggtggca 780  
gatatagttc atgcttggtt acaaattgat cctgctgaca ggatatcatc tagtgatctt 840  
ttgcatcatg agtattttac tagagatgga tttattgaaa aattcatgcc agaactgaaa 900  
gctaaattac tgcaggaagc aaaagtcaat tcattaataa agccaaaaga gaggttctaaa 960  
gaaaatgaac tcaggaaga tgaaagaaaa acagtttata ccaatacact gctaagtagt 1020  
tcagttttgg gagaggaaat agaaaaagag aaaaagccca aggagatcaa agtcagagtt 1080  
attaaagtca aaggaggaag aggagatata tcagaaccaa aaaagaaaga gtatgaagg 1140  
ggacttggtc aacaggatgc aaatgaaaaat gttcatccta tgtctccaga tacaaaactt 1200  
gtaaccattg aaccaccaa ccctatcaat ccagcacta actgtaatgg cttgaaagaa 1260  
aatccacatt gcggaggttc tgtaacaatg ccacccatca atctaactaa cagtaatttg 1320  
atggctgcaa atctcagttc aaatctcttt cccccagtg tgagggtgagc tgtaacagag 1380  
aagaaaccta aataatacaa cattcctgta taatgggtatt tcaaagaatc gtgttcatag 1440  
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aaaaaaaaaaa aaa 1513

<210> 34  
 <211> 455  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <223> serine threonine protein kinase NKIAMRE,  
 mitogen-activated protein kinase/cyclin-dependent  
 kinase-related protein kinase NKIATRE homologue  
  
 <400> 34  
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 Thr Val Met Lys Cys Lys His Lys Asn Thr Gly Gln Ile Val Ala Ile  
 20 25 30  
 Lys Ile Phe Tyr Glu Arg Pro Glu Gln Ser Val Asn Lys Ile Ala Met  
 35 40 45  
 Arg Glu Ile Lys Phe Leu Lys Gln Phe His His Glu Asn Leu Val Asn  
 50 55 60  
 Leu Ile Glu Val Phe Arg Gln Lys Lys Lys Ile His Leu Val Phe Glu  
 65 70 75 80  
 Phe Ile Asp His Thr Val Leu Asp Glu Leu Gln His Tyr Cys His Gly  
 85 90 95  
 Leu Glu Ser Lys Arg Leu Arg Lys Tyr Leu Phe Gln Ile Leu Arg Ala  
 100 105 110  
 Ile Asp Tyr Leu His Ser Asn Asn Ile Ile His Arg Asp Ile Lys Pro  
 115 120 125  
 Glu Asn Ile Leu Val Ser Gln Ser Gly Ile Thr Lys Leu Cys Asp Phe  
 130 135 140  
 Gly Phe Ala Arg Thr Leu Ala Ala Pro Gly Asp Ile Tyr Thr Asp Tyr  
 145 150 155 160  
 Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Val Leu Lys Asp Thr  
 165 170 175  
 Ser Tyr Gly Lys Pro Val Asp Ile Trp Ala Leu Gly Cys Met Ile Ile  
 180 185 190  
 Glu Met Ala Thr Gly Asn Pro Tyr Leu Pro Ser Ser Ser Asp Leu Asp  
 195 200 205  
 Leu Leu His Lys Ile Val Leu Lys Val Gly Asn Leu Ser Pro His Leu  
 210 215 220  
 Gln Asn Ile Phe Ser Lys Ser Pro Ile Phe Ala Gly Val Val Leu Pro  
 225 230 235 240  
 Gln Val Gln His Pro Lys Asn Ala Arg Lys Lys Tyr Pro Lys Leu Asn  
 245 250 255  
 Gly Leu Leu Ala Asp Ile Val His Ala Cys Leu Gln Ile Asp Pro Ala  
 260 265 270

Asp Arg Ile Ser Ser Ser Asp Leu Leu His His Glu Tyr Phe Thr Arg  
 275 280 285  
 Asp Gly Phe Ile Glu Lys Phe Met Pro Glu Leu Lys Ala Lys Leu Leu  
 290 295 300  
 Gln Glu Ala Lys Val Asn Ser Leu Ile Lys Pro Lys Glu Ser Ser Lys  
 305 310 315 320  
 Glu Asn Glu Leu Arg Lys Asp Glu Arg Lys Thr Val Tyr Thr Asn Thr  
 325 330 335  
 Leu Leu Ser Ser Ser Val Leu Gly Glu Glu Ile Glu Lys Glu Lys Lys  
 340 345 350  
 Pro Lys Glu Ile Lys Val Arg Val Ile Lys Val Lys Gly Gly Arg Gly  
 355 360 365  
 Asp Ile Ser Glu Pro Lys Lys Lys Glu Tyr Glu Gly Gly Leu Gly Gln  
 370 375 380  
 Gln Asp Ala Asn Glu Asn Val His Pro Met Ser Pro Asp Thr Lys Leu  
 385 390 395 400  
 Val Thr Ile Glu Pro Pro Asn Pro Ile Asn Pro Ser Thr Asn Cys Asn  
 405 410 415  
 Gly Leu Lys Glu Asn Pro His Cys Gly Gly Ser Val Thr Met Pro Pro  
 420 425 430  
 Ile Asn Leu Thr Asn Ser Asn Leu Met Ala Ala Asn Leu Ser Ser Asn  
 435 440 445  
 Leu Phe His Pro Ser Val Arg  
 450 455

<210> 35

<211> 3504

<212> DNA

<213> Homo sapiens

<220>

<223> HB01 histone acetyltransferase, MYST histone  
acetyltransferase 2 (MYST2)

<400> 35

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aatgcaggca gtagttcaga tggaaccgaa gattccgatt tttctacaga tctcgagcac 120
acagacagtt cagaaagtga tggcacatcc cgacgatctg ctcgagtcac ccgctcctca 180
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actgaggagc ctgcttactc taccagaaga gtgaccgcta gtcagcagca gcctacccca 300
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gtgggttgatt tttcagatag agaaactaaa aatacagctg atcatgatga gtcaccgcct 420
cgaactccaa ctggaaaatgc gccttcttct gagtctgaca tagatatctc cagccccaat 480
gtatctcacg atgagagcat tgccaaggac atgtccctga aggactcagg cagtgatctc 540
tctcatcgcc ccaagcgccg tcgcttccat gaaagctaca acttcaatat gaagtgtcct 600
acaccaggct gtaactctct aggacacctt acaggaaaac atgagagaca tttctccatc 660
tcaggatgcc cactgtatca taacctctca gctgacgaat gcaagggtgag agcacagagc 720
cgggataagc agatagaaga aaggatgctg tctcacaggc aagatgacaa caacaggcat 780
gcaaccaggc accaggcacc aacggagagg cagcttcgat ataaggaaaa agtggctgaa 840
  
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Asp	Ser	Asp	Phe	Ser	Thr	Asp	Leu	Glu	His	Thr	Asp	Ser	Ser	Glu	Ser	20	25	30	
Asp	Gly	Thr	Ser	Arg	Arg	Ser	Ala	Arg	Val	Thr	Arg	Ser	Ser	Ala	Arg	35	40	45	
Leu	Ser	Gln	Ser	Ser	Gln	Asp	Ser	Ser	Pro	Val	Arg	Asn	Leu	Gln	Ser	50	55	60	
Phe	Gly	Thr	Glu	Glu	Pro	Ala	Tyr	Ser	Thr	Arg	Arg	Val	Thr	Arg	Ser	65	70	75	80
Gln	Gln	Gln	Pro	Thr	Pro	Val	Thr	Pro	Lys	Lys	Tyr	Pro	Leu	Arg	Gln	85	90	95	
Thr	Arg	Ser	Ser	Gly	Ser	Glu	Thr	Glu	Gln	Val	Val	Asp	Phe	Ser	Asp	100	105	110	
Arg	Glu	Thr	Lys	Asn	Thr	Ala	Asp	His	Asp	Glu	Ser	Pro	Pro	Arg	Thr	115	120	125	
Pro	Thr	Gly	Asn	Ala	Pro	Ser	Ser	Glu	Ser	Asp	Ile	Asp	Ile	Ser	Ser	130	135	140	
Pro	Asn	Val	Ser	His	Asp	Glu	Ser	Ile	Ala	Lys	Asp	Met	Ser	Leu	Lys	145	150	155	160
Asp	Ser	Gly	Ser	Asp	Leu	Ser	His	Arg	Pro	Lys	Arg	Arg	Arg	Phe	His	165	170	175	
Glu	Ser	Tyr	Asn	Phe	Asn	Met	Lys	Cys	Pro	Thr	Pro	Gly	Cys	Asn	Ser	180	185	190	
Leu	Gly	His	Leu	Thr	Gly	Lys	His	Glu	Arg	His	Phe	Ser	Ile	Ser	Gly	195	200	205	
Cys	Pro	Leu	Tyr	His	Asn	Leu	Ser	Ala	Asp	Glu	Cys	Lys	Val	Arg	Ala	210	215	220	
Gln	Ser	Arg	Asp	Lys	Gln	Ile	Glu	Glu	Arg	Met	Leu	Ser	His	Arg	Gln	225	230	235	240
Asp	Asp	Asn	Asn	Arg	His	Ala	Thr	Arg	His	Gln	Ala	Pro	Thr	Glu	Arg	245	250	255	
Gln	Leu	Arg	Tyr	Lys	Glu	Lys	Val	Ala	Glu	Leu	Arg	Lys	Lys	Arg	Asn	260	265	270	
Ser	Gly	Leu	Ser	Lys	Glu	Gln	Lys	Glu	Lys	Tyr	Met	Glu	His	Arg	Gln	275	280	285	
Thr	Tyr	Gly	Asn	Thr	Arg	Glu	Pro	Leu	Leu	Glu	Asn	Leu	Thr	Ser	Glu	290	295	300	
Tyr	Asp	Leu	Asp	Leu	Phe	Arg	Arg	Ala	Gln	Ala	Arg	Ala	Ser	Glu	Asp	305	310	315	320
Leu	Glu	Lys	Leu	Arg	Leu	Gln	Gly	Gln	Ile	Thr	Glu	Gly	Ser	Asn	Met	325	330	335	

Ile	Lys	Thr	Ile	Ala	Phe	Gly	Arg	Tyr	Glu	Leu	Asp	Thr	Trp	Tyr	His	340	345	350	
Ser	Pro	Tyr	Pro	Glu	Glu	Tyr	Ala	Arg	Leu	Gly	Arg	Leu	Tyr	Met	Cys	355	360	365	
Glu	Phe	Cys	Leu	Lys	Tyr	Met	Lys	Ser	Gln	Thr	Ile	Leu	Arg	Arg	His	370	375	380	
Met	Ala	Lys	Cys	Val	Trp	Lys	His	Pro	Pro	Gly	Asp	Glu	Ile	Tyr	Arg	385	390	395	400
Lys	Gly	Ser	Ile	Ser	Val	Phe	Glu	Val	Asp	Gly	Lys	Lys	Asn	Lys	Ile	405	410	415	
Tyr	Cys	Gln	Asn	Leu	Cys	Leu	Leu	Ala	Lys	Leu	Phe	Leu	Asp	His	Lys	420	425	430	
Thr	Leu	Tyr	Tyr	Asp	Val	Glu	Pro	Phe	Leu	Phe	Tyr	Val	Met	Thr	Glu	435	440	445	
Ala	Asp	Asn	Thr	Gly	Cys	His	Leu	Ile	Gly	Tyr	Phe	Ser	Lys	Glu	Lys	450	455	460	
Asn	Ser	Phe	Leu	Asn	Tyr	Asn	Val	Ser	Cys	Ile	Leu	Thr	Met	Pro	Gln	465	470	475	480
Tyr	Met	Arg	Gln	Gly	Tyr	Gly	Lys	Met	Leu	Ile	Asp	Phe	Ser	Tyr	Leu	485	490	495	
Leu	Ser	Lys	Val	Glu	Glu	Lys	Val	Gly	Ser	Pro	Glu	Arg	Pro	Leu	Ser	500	505	510	
Asp	Leu	Gly	Leu	Ile	Ser	Tyr	Arg	Ser	Tyr	Trp	Lys	Glu	Val	Leu	Leu	515	520	525	
Arg	Tyr	Leu	His	Asn	Phe	Gln	Gly	Lys	Glu	Ile	Ser	Ile	Lys	Glu	Ile	530	535	540	
Ser	Gln	Glu	Thr	Ala	Val	Asn	Pro	Val	Asp	Ile	Val	Ser	Thr	Leu	Gln	545	550	555	560
Ala	Leu	Gln	Met	Leu	Lys	Tyr	Trp	Lys	Gly	Lys	His	Leu	Val	Leu	Lys	565	570	575	
Arg	Gln	Asp	Leu	Ile	Asp	Glu	Trp	Ile	Ala	Lys	Glu	Ala	Lys	Arg	Ser	580	585	590	
Asn	Ser	Asn	Lys	Thr	Met	Asp	Pro	Ser	Cys	Leu	Lys	Trp	Thr	Pro	Pro	595	600	605	
Lys	Gly	Thr														610			

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CK2-specific  
 siRNA molecule

<400> 37  
 aacattgaat tagatccacg t 21

<210> 38  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:PIM1-specific  
 siRNA molecule

<400> 38  
 aaaactccga gtgaactggt c 21

<210> 39  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HBO1-specific  
 siRNA molecule

<400> 39  
 aactgagcaa gtggttgatt t 21

<210> 40  
 <211> 409  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> CDC7 cell division cycle 7 (CDC7), CDC7 cell  
 division cycle 7-like 1 (CDC7L1) protein serine  
 threonine kinase

<400> 40  
 Met Glu Ala Ser Leu Gly Ile Gln Met Asp Glu Pro Met Ala Phe Ser  
 1 5 10 15  
 Pro Gln Arg Asp Arg Phe Gln Ala Glu Gly Ser Leu Lys Lys Asn Glu  
 20 25 30  
 Gln Asn Phe Lys Leu Ala Gly Val Lys Lys Asp Ile Glu Lys Leu Tyr  
 35 40 45  
 Glu Ala Val Pro Gln Leu Ser Asn Val Phe Lys Ile Glu Asp Lys Ile  
 50 55 60  
 Gly Glu Gly Thr Phe Ser Ser Val Tyr Leu Ala Thr Ala Gln Leu Gln  
 65 70 75 80

Val	Gly	Pro	Glu	Glu	Lys	Ile	Ala	Leu	Lys	His	Leu	Ile	Pro	Thr	Ser	
				85					90						95	
His	Pro	Ile	Arg	Ile	Ala	Ala	Glu	Leu	Gln	Cys	Leu	Thr	Val	Ala	Gly	
			100					105						110		
Gly	Gln	Asp	Asn	Val	Met	Gly	Val	Lys	Tyr	Cys	Phe	Arg	Lys	Asn	Asp	
		115					120					125				
His	Val	Val	Ile	Ala	Met	Pro	Tyr	Leu	Glu	His	Glu	Ser	Phe	Leu	Asp	
	130					135					140					
Ile	Leu	Asn	Ser	Leu	Ser	Phe	Gln	Glu	Val	Arg	Glu	Tyr	Met	Leu	Asn	
145					150					155					160	
Leu	Phe	Lys	Ala	Leu	Lys	Arg	Ile	His	Gln	Phe	Gly	Ile	Val	His	Arg	
				165					170					175		
Asp	Val	Lys	Pro	Ser	Asn	Phe	Leu	Tyr	Asn	Arg	Arg	Leu	Lys	Lys	Tyr	
			180					185					190			
Ala	Leu	Val	Asp	Phe	Gly	Leu	Ala	Gln	Gly	Thr	His	Asp	Thr	Lys	Ile	
		195					200					205				
Glu	Leu	Leu	Lys	Phe	Val	Gln	Ser	Glu	Ala	Gln	Gln	Glu	Arg	Cys	Ser	
	210					215						220				
Gln	Asn	Lys	Ser	His	Ile	Ile	Thr	Gly	Asn	Lys	Ile	Pro	Leu	Ser	Gly	
225					230					235					240	
Pro	Val	Pro	Lys	Glu	Leu	Asp	Gln	Gln	Ser	Thr	Thr	Lys	Ala	Ser	Val	
				245					250					255		
Lys	Arg	Pro	Tyr	Thr	Asn	Ala	Gln	Ile	Gln	Ile	Lys	Gln	Gly	Lys	Asp	
			260					265					270			
Gly	Lys	Glu	Gly	Ser	Val	Gly	Leu	Ser	Val	Gln	Arg	Ser	Val	Phe	Gly	
		275					280					285				
Glu	Arg	Asn	Phe	Asn	Ile	His	Ser	Ser	Ile	Ser	His	Glu	Ser	Pro	Ala	
	290					295					300					
Val	Lys	Leu	Met	Lys	Gln	Ser	Lys	Thr	Val	Asp	Val	Leu	Ser	Arg	Lys	
305					310					315					320	
Leu	Ala	Thr	Lys	Lys	Lys	Ala	Ile	Ser	Thr	Lys	Val	Met	Asn	Ser	Ala	
				325					330					335		
Val	Met	Arg	Lys	Thr	Ala	Ser	Ser	Cys	Pro	Ala	Ser	Leu	Thr	Cys	Asp	
			340					345					350			
Cys	Tyr	Ala	Thr	Asp	Lys	Val	Cys	Ser	Ile	Cys	Leu	Ser	Arg	Arg	Gln	
		355					360					365				
Gln	Val	Ala	Pro	Arg	Ala	Gly	Thr	Pro	Gly	Phe	Arg	Ala	Pro	Glu	Val	
	370					375					380					

Leu Thr Lys Cys Pro Asn Gln Thr Thr Ala Ile Asp Met Trp Ser Ala  
 385 390 395 400

Gly Val Ile Phe Leu Ser Leu Leu Ser  
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<210> 41  
 <211> 314  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<220>  
 <223> CDC7

<400> 41  
 Met Thr Ser Lys Thr Lys Asn Ile Asp Asp Ile Pro Pro Glu Ile Lys  
 1 5 10 15

Glu Glu Met Ile Gln Leu Tyr His Asp Leu Pro Gly Ile Glu Asn Glu  
 20 25 30

Tyr Lys Leu Ile Asp Lys Ile Gly Glu Gly Thr Phe Ser Ser Val Tyr  
 35 40 45

Lys Ala Lys Asp Ile Thr Gly Lys Ile Thr Lys Lys Phe Ala Ser His  
 50 55 60

Phe Trp Asn Tyr Gly Ser Asn Tyr Val Ala Leu Lys Lys Ile Tyr Val  
 65 70 75 80

Thr Ser Ser Pro Gln Arg Ile Tyr Asn Glu Leu Asn Leu Leu Tyr Ile  
 85 90 95

Met Thr Gly Ser Ser Arg Val Ala Pro Leu Cys Asp Ala Lys Arg Val  
 100 105 110

Arg Asp Gln Val Ile Ala Val Leu Pro Tyr Tyr Pro His Glu Glu Phe  
 115 120 125

Arg Thr Phe Tyr Arg Asp Leu Pro Ile Lys Gly Ile Lys Lys Tyr Ile  
 130 135 140

Trp Glu Leu Leu Arg Ala Leu Lys Phe Val His Ser Lys Gly Ile Ile  
 145 150 155 160

His Arg Asp Ile Lys Pro Thr Asn Phe Leu Phe Asn Leu Glu Leu Gly  
 165 170 175

Arg Gly Val Leu Val Asp Phe Gly Leu Ala Glu Ala Gln Met Asp Tyr  
 180 185 190

Lys Ser Met Ile Ser Ser Gln Asn Asp Tyr Asp Asn Tyr Ala Asn Thr  
 195 200 205

Asn His Asp Gly Gly Tyr Ser Met Arg Asn His Glu Gln Phe Cys Pro  
 210 215 220

Cys Ile Met Arg Asn Gln Tyr Ser Pro Asn Ser His Asn Gln Thr Pro  
 225 230 235 240

Pro Met Val Thr Ile Gln Asn Gly Lys Val Val His Leu Asn Asn Val  
245 250 255

Asn Gly Val Asp Leu Thr Lys Gly Tyr Pro Lys Asn Glu Thr Arg Arg  
260 265 270

Ile Lys Arg Ala Asn Arg Ala Gly Thr Arg Gly Phe Arg Ala Pro Glu  
275 280 285

Val Leu Met Lys Cys Gly Ala Gln Ser Thr Lys Ile Asp Ile Trp Ser  
290 295 300

Val Gly Val Ile Leu Leu Ser Leu Leu Gly  
305 310

<210> 42

<211> 294

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:protein kinase  
consensus sequence

<400> 42

Tyr Glu Leu Leu Glu Lys Leu Gly Glu Gly Ser Phe Gly Lys Val Tyr  
1 5 10 15

Lys Ala Lys His Lys Asp Lys Thr Gly Lys Ile Val Ala Val Lys Ile  
20 25 30

Leu Lys Lys Glu Lys Glu Ser Ile Lys Glu Lys Arg Phe Leu Arg Glu  
35 40 45

Ile Gln Ile Leu Lys Arg Leu Ser His Pro Asn Ile Val Arg Leu Ile  
50 55 60

Gly Val Phe Glu Asp Thr Asp Asp His Leu Tyr Leu Val Met Glu Tyr  
65 70 75 80

Met Glu Gly Gly Asp Leu Phe Asp Tyr Leu Arg Arg Asn Gly Gly Pro  
85 90 95

Leu Ser Glu Lys Glu Ala Lys Lys Ile Ala Leu Gln Ile Leu Arg Gly  
100 105 110

Leu Glu Tyr Leu His Ser Asn Gly Ile Val His Arg Asp Leu Lys Pro  
115 120 125

Glu Asn Ile Leu Leu Asp Glu Asn Asp Gly Thr Val Lys Ile Ala Asp  
130 135 140

Phe Gly Leu Ala Arg Leu Leu Glu Ser Ser Ser Lys Leu Thr Thr Phe  
145 150 155 160

Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile Leu Glu Gly  
165 170 175

Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly Val Ile Leu  
180 185 190

Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala Asp Leu Pro  
 195 200 205  
 Ala Phe Thr Gly Gly Asp Glu Val Asp Gln Leu Ile Ile Phe Val Leu  
 210 215 220  
 Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile Asp Pro Leu  
 225 230 235 240  
 Glu Glu Leu Phe Arg Ile Ile Lys Arg Pro Gly Leu Arg Leu Pro Leu  
 245 250 255  
 Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Lys Cys Leu  
 260 265 270  
 Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr Ala Lys Glu Ile  
 275 280 285  
 Leu Asn His Pro Trp Phe  
 290

<210> 43  
 <211> 253  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> cytokine-inducible kinase (CNK) serine threonine  
 kinase, proliferation-related kinase (PRK),  
 polo-like kinase 3 (PLK3)

<400> 43  
 Tyr Leu Lys Gly Arg Leu Leu Gly Lys Gly Gly Phe Ala Arg Cys Tyr  
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 20 25 30  
 Pro Gln Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Leu Asn  
 35 40 45  
 Glu Ile Glu Leu His Arg Asp Leu Gln His Arg His Ile Val Arg Phe  
 50 55 60  
 Ser His His Phe Glu Asp Ala Asp Asn Ile Tyr Ile Phe Leu Glu Leu  
 65 70 75 80  
 Cys Ser Arg Lys Ser Leu Ala His Ile Trp Lys Ala Arg His Thr Leu  
 85 90 95  
 Leu Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Leu Ser Gly Leu  
 100 105 110  
 Lys Tyr Leu His Gln Arg Gly Ile Leu His Arg Asp Leu Lys Leu Gly  
 115 120 125  
 Asn Phe Phe Ile Thr Glu Asn Met Glu Leu Lys Val Gly Asp Phe Gly  
 130 135 140

Leu	Ala	Ala	Arg	Leu	Glu	Pro	Pro	Glu	Gln	Arg	Lys	Lys	Thr	Ile	Cys	
145					150					155					160	
Gly	Thr	Pro	Asn	Tyr	Val	Ala	Pro	Glu	Val	Leu	Leu	Arg	Gln	Gly	His	
			165						170					175		
Gly	Pro	Glu	Ala	Asp	Val	Trp	Ser	Leu	Gly	Cys	Val	Met	Tyr	Thr	Leu	
			180					185					190			
Leu	Cys	Gly	Ser	Pro	Pro	Phe	Glu	Thr	Ala	Asp	Leu	Lys	Glu	Thr	Tyr	
		195					200					205				
Arg	Cys	Ile	Lys	Gln	Val	His	Tyr	Thr	Leu	Pro	Ala	Ser	Leu	Ser	Leu	
	210					215					220					
Pro	Ala	Arg	Gln	Leu	Leu	Ala	Ala	Ile	Leu	Arg	Ala	Ser	Pro	Arg	Asp	
225				230						235					240	
Arg	Pro	Ser	Ile	Asp	Gln	Ile	Leu	Arg	His	Asp	Phe	Phe				
				245					250							

<210> 44  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:consensus peptide

<400> 44  
 His Arg Asp Leu Lys  
 1 5

<210> 45  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:consensus peptide

<400> 45  
 Asp Phe Gly Leu Ala  
 1 5

<210> 46  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:consensus peptide



<400> 46  
 Ala Pro Glu Val  
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<210> 47  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:consensus  
 peptide

<400> 47  
 Asp Val Trp Ser Leu Gly  
 1 5

<210> 48  
 <211> 256  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> serine threonine kinase 2 (STK2, NEK4)

<400> 48  
 Tyr Cys Tyr Leu Arg Val Val Gly Lys Gly Ser Tyr Gly Glu Val Thr  
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 Leu Val Lys His Arg Arg Asp Gly Lys Gln Tyr Val Ile Lys Lys Leu  
 20 25 30  
 Asn Leu Arg Asn Ala Ser Ser Arg Glu Arg Arg Ala Ala Glu Gln Glu  
 35 40 45  
 Ala Gln Leu Leu Ser Gln Leu Lys His Pro Asn Ile Val Thr Tyr Lys  
 50 55 60  
 Glu Ser Trp Glu Gly Gly Asp Gly Leu Leu Tyr Ile Val Met Gly Phe  
 65 70 75 80  
 Cys Glu Gly Gly Asp Leu Tyr Arg Lys Leu Lys Glu Gln Lys Gly Gln  
 85 90 95  
 Leu Leu Pro Glu Asn Gln Val Val Glu Trp Phe Val Gln Ile Ala Met  
 100 105 110  
 Ala Leu Gln Tyr Leu His Glu Lys His Ile Leu His Arg Asp Leu Lys  
 115 120 125  
 Thr Gln Asn Val Phe Leu Thr Arg Thr Asn Ile Ile Lys Val Gly Asp  
 130 135 140  
 Leu Gly Ile Ala Arg Val Leu Glu Asn His Cys Asp Met Ala Ser Thr  
 145 150 155 160  
 Leu Ile Gly Thr Pro Tyr Tyr Met Ser Pro Glu Leu Phe Ser Asn Lys  
 165 170 175

Pro	Tyr	Asn	Tyr	Lys	Ser	Asp	Val	Trp	Ala	Leu	Gly	Cys	Cys	Val	Tyr
			180					185					190		
Glu	Met	Ala	Thr	Leu	Lys	His	Ala	Phe	Asn	Ala	Lys	Asp	Met	Asn	Ser
		195					200					205			
Leu	Val	Tyr	Arg	Ile	Ile	Glu	Gly	Lys	Leu	Pro	Pro	Met	Pro	Arg	Asp
	210					215					220				
Tyr	Ser	Pro	Glu	Leu	Ala	Glu	Leu	Ile	Arg	Thr	Met	Leu	Ser	Lys	Arg
225					230					235					240
Pro	Glu	Glu	Arg	Pro	Ser	Val	Arg	Ser	Ile	Leu	Arg	Gln	Pro	Tyr	Ile
			245						250					255	

<210> 49  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:consensus  
 peptide

<400> 49  
 His Pro Asn Ile Val  
 1 5

<210> 50  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:consensus  
 peptide

<400> 50  
 Glu Gly Gly Asp Leu  
 1 5

<210> 51  
 <211> 294  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:protein kinase  
 consensus sequence

<400> 51  
 Tyr Glu Leu Leu Glu Lys Leu Gly Glu Gly Ser Phe Gly Lys Val Tyr  
 1 5 10 15  
 Lys Ala Lys His Lys Asp Lys Thr Gly Lys Ile Val Ala Val Lys Ile  
 20 25 30

Leu Lys Lys Glu Lys Glu Ser Ile Lys Glu Lys Arg Phe Leu Arg Glu  
                   35                                  40                                  45  
 Ile Gln Ile Leu Lys Arg Leu Ser His Pro Asn Ile Val Arg Leu Ile  
           50                                  55                                  60  
 Gly Val Phe Glu Asp Thr Asp Asp His Leu Tyr Leu Val Met Glu Tyr  
   65                                  70                                  75                                  80  
 Met Glu Gly Gly Asp Leu Phe Asp Tyr Leu Arg Arg Asn Gly Gly Pro  
                                   85                                  90                                  95  
 Leu Ser Glu Lys Glu Ala Lys Lys Ile Ala Leu Gln Ile Leu Arg Gly  
                   100                                  105                                  110  
 Leu Glu Tyr Leu His Ser Asn Gly Ile Val His Arg Asp Leu Lys Pro  
           115                                  120                                  125  
 Glu Asn Ile Leu Leu Asp Glu Asn Asp Gly Thr Val Lys Ile Ala Asp  
   130                                  135                                  140  
 Phe Gly Leu Ala Arg Leu Leu Glu Ser Ser Ser Lys Leu Thr Thr Phe  
  145                                  150                                  155                                  160  
 Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile Leu Glu Gly  
                   165                                  170                                  175  
 Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly Val Ile Leu  
           180                                  185                                  190  
 Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala Asp Leu Pro  
   195                                  200                                  205  
 Ala Phe Thr Gly Gly Asp Glu Val Asp Gln Leu Ile Ile Phe Val Leu  
   210                                  215                                  220  
 Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile Asp Pro Leu  
  225                                  230                                  235                                  240  
 Glu Glu Leu Phe Arg Ile Ile Lys Arg Pro Gly Leu Arg Leu Pro Leu  
                   245                                  250                                  255  
 Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Lys Cys Leu  
           260                                  265                                  270  
 Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr Ala Lys Glu Ile  
   275                                  280                                  285  
 Leu Asn His Pro Trp Phe  
   290

<210> 52

<211> 286

<212> PRT

<213> Homo sapiens

<220>

<223> serine threonine protein kinase casein kinase 2,  
       alpha 1 subunit isoform a, transcript variant 2  
       (CK2, CK2alpha), CK2 catalytic subunit alpha

<400> 52  
Tyr Gln Leu Val Arg Lys Leu Gly Arg Gly Lys Tyr Ser Glu Val Phe  
1 5 10 15  
Glu Ala Ile Asn Ile Thr Asn Asn Glu Lys Val Val Val Lys Ile Leu  
20 25 30  
Lys Pro Val Lys Lys Lys Lys Ile Lys Arg Glu Ile Lys Ile Leu Glu  
35 40 45  
Asn Leu Arg Gly Gly Pro Asn Ile Ile Thr Leu Ala Asp Ile Val Lys  
50 55 60  
Asp Pro Val Ser Arg Thr Pro Ala Leu Val Phe Glu His Val Asn Asn  
65 70 75 80  
Thr Asp Phe Lys Gln Leu Tyr Gln Thr Leu Thr Asp Tyr Asp Ile Arg  
85 90 95  
Phe Tyr Met Tyr Glu Ile Leu Lys Ala Leu Asp Tyr Cys His Ser Met  
100 105 110  
Gly Ile Met His Arg Asp Val Lys Pro His Asn Val Met Ile Asp His  
115 120 125  
Glu His Arg Lys Leu Arg Leu Ile Asp Trp Gly Leu Ala Glu Phe Tyr  
130 135 140  
His Pro Gly Gln Glu Tyr Asn Val Arg Val Ala Ser Arg Tyr Phe Lys  
145 150 155 160  
Gly Pro Glu Leu Leu Val Asp Tyr Gln Met Tyr Asp Tyr Ser Leu Asp  
165 170 175  
Met Trp Ser Leu Gly Cys Met Leu Ala Ser Met Ile Phe Arg Lys Glu  
180 185 190  
Pro Phe Phe His Gly His Asp Asn Tyr Asp Gln Leu Val Arg Ile Ala  
195 200 205  
Lys Val Leu Gly Thr Glu Asp Leu Tyr Asp Tyr Ile Asp Lys Tyr Asn  
210 215 220  
Ile Glu Leu Asp Pro Arg Phe Asn Asp Ile Leu Gly Arg His Ser Arg  
225 230 235 240  
Lys Arg Trp Glu Arg Phe Val His Ser Glu Asn Gln His Leu Val Ser  
245 250 255  
Pro Glu Ala Leu Asp Phe Leu Asp Lys Leu Leu Arg Tyr Asp His Gln  
260 265 270  
Ser Arg Leu Thr Ala Arg Glu Ala Met Glu His Pro Tyr Phe  
275 280 285

<210> 53  
<211> 5  
<212> PRT  
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 53
Val Lys Ile Leu Lys
  1             5

<210> 54
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 54
Trp Ser Leu Gly
  1

<210> 55
<211> 298
<212> PRT
<213> Homo sapiens

<220>
<223> cyclin-dependent kinase 2 (CDK2)

<400> 55
Met Glu Asn Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly
  1             5             10             15

Val Val Tyr Lys Ala Arg Asn Lys Leu Thr Gly Glu Val Val Ala Leu
          20             25             30

Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu Gly Val Pro Ser Thr Ala
          35             40             45

Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Asn His Pro Asn Ile Val
          50             55             60

Lys Leu Leu Asp Val Ile His Thr Glu Asn Lys Leu Tyr Leu Val Phe
          65             70             75             80

Glu Phe Leu His Gln Asp Leu Lys Lys Phe Met Asp Ala Ser Ala Leu
          85             90             95

Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu
          100            105            110

Gln Gly Leu Ala Phe Cys His Ser His Arg Val Leu His Arg Asp Leu
          115            120            125

Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu Gly Ala Ile Lys Leu Ala
          130            135            140

Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Val Arg Thr Tyr Thr
          145            150            155            160

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<210> 57  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> flap structure-specific endonuclease 1 (FEN1)  
 5'-3' exonuclease

<400> 57  
 Met Gly Ile Gln Gly Leu Ala Lys Leu Ile Ala Asp Val Ala Pro Ser  
   1                  5                  10                  15  
 Ala Ile Arg Glu Asn Asp Ile Lys Ser Tyr Phe Gly Arg Lys Val Ala  
           20                  25                  30  
 Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln  
       35                  40                  45  
 Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser His Leu  
       50                  55                  60  
 Met Gly Met Phe Tyr Arg Thr Ile Arg Met Met Glu Asn Gly Ile Lys  
       65                  70                  75                  80  
 Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu  
                   85                  90                  95  
 Leu Ala Lys Arg Ser Glu Arg Arg Ala Glu Ala  
       100                  105

<210> 58  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:consensus  
 peptide

<400> 58  
 Ala Ile Asp Ala Ser  
   1                  5

<210> 59  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:consensus  
 peptide

<400> 59  
 Tyr Gln Phe Leu  
   1

<210> 60  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide

<400> 60  
Asn Glu Glu Gly Glu Thr Thr Ser His Leu Met Gly  
1 5 10

<210> 61  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide

<400> 61  
Gly Ile Lys Pro  
1

<210> 62  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide

<400> 62  
Val Phe Asp Gly  
1

<210> 63  
<211> 104  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Xeroderma  
pigmentosum complementation group XPG I-region  
domain (XPG\_I) consensus sequence

<400> 63  
Arg Leu Met Gly Ile Pro Tyr Ile Val Ala Pro Gly Val Glu Ala Glu  
1 5 10 15

Ala Gln Cys Ala Tyr Leu Glu Lys Lys Gly Leu Val Asp Gly Ile Ile  
20 25 30

Thr Glu Asp Ser Asp Val Leu Leu Phe Gly Ala Pro Arg Leu Leu Arg  
35 40 45



Asn Leu Thr Leu Ser Gly Lys Lys Ser Gly Pro Ser Ile Thr Ser Leu  
     50                    55                    60  
 Lys Val Glu Ile Glu Glu Ile Asp Leu Glu Ser Leu Leu Arg Glu Leu  
     65                    70                    75                    80  
 Gly Leu Gly Lys Leu Ser Arg Glu Gln Leu Ile Asp Leu Ala Ile Leu  
                     85                    90                    95  
 Leu Gly Cys Asp Tyr Thr Glu Gly  
                     100

<210> 64  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> flap structure-specific endonuclease 1 (FEN1)  
       5'-3' exonuclease

<400> 64  
 Ser Leu Met Gly Ile Pro Tyr Leu Asp Ala Pro Ser Glu Ala Glu Ala  
     1                    5                    10                    15  
 Ser Cys Ala Ala Leu Val Lys Ala Gly Lys Val Tyr Ala Ala Ala Thr  
                     20                    25                    30  
 Glu Asp Met Asp Cys Leu Thr Phe Gly Ser Pro Val Leu Met Arg His  
     35                    40                    45  
 Leu Thr Ala Ser Glu Ala Lys Lys Leu Pro Ile Gln Glu Phe His Leu  
     50                    55                    60  
 Ser Arg Ile Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val Asp  
     65                    70                    75                    80  
 Leu Cys Ile Leu Leu Gly Ser Asp Tyr Cys Glu Ser  
                     85                    90

<210> 65  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:consensus  
       peptide

<400> 65  
 Leu Met Gly Ile Pro Tyr  
     1                    5

<210> 66  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 66
Glu Ala Glu Ala
  1

<210> 67
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 67
Glu Leu Gly Leu
  1

<210> 68
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 68
Ile Leu Leu Gly
  1

<210> 69
<211> 261
<212> PRT
<213> Homo sapiens

<220>
<223> HBO1 histone acetyltransferase, MYST histone
      acetyltransferase 2 (MYST2)

<400> 69
Tyr His Ser Pro Tyr Pro Glu Glu Tyr Ala Arg Leu Gly Arg Leu Tyr
  1             5             10             15
Met Cys Glu Phe Cys Leu Lys Tyr Met Lys Ser Gln Thr Ile Leu Arg
          20             25             30
Arg His Met Ala Lys Cys Val Trp Lys His Pro Pro Gly Asp Glu Ile
          35             40             45
Tyr Arg Lys Gly Ser Ile Ser Val Phe Glu Val Asp Gly Lys Lys Asn
          50             55             60
Lys Ile Tyr Cys Gln Asn Leu Cys Leu Leu Ala Lys Leu Phe Leu Asp
          65             70             75             80

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Leu	Ile	Leu	Glu	Arg	Pro	Glu	Pro	Val	Gln	Asp	Leu	Phe	Asp	Phe	Ile
				85					90					95	
Thr	Glu	Arg	Gly	Ala	Leu	Gln	Glu	Glu	Leu	Ala	Arg	Ser	Phe	Phe	Trp
			100					105					110		
Gln	Val	Leu	Glu	Ala	Val	Arg	His	Cys	His	Asn	Cys	Gly	Val	Leu	His
		115					120					125			
Arg	Asp	Ile	Lys	Asp	Glu	Asn	Ile	Leu	Ile	Asp	Leu	Asn	Arg	Gly	Glu
	130					135					140				
Leu	Lys	Leu	Ile	Asp	Phe	Gly	Ser	Gly	Ala	Leu	Leu	Lys	Asp	Thr	Val
145					150					155					160
Tyr	Thr	Asp	Phe	Asp	Gly	Thr	Arg	Val	Tyr	Ser	Pro	Pro	Glu	Trp	Ile
			165						170					175	
Arg	Tyr	His	Arg	Tyr	His	Gly	Arg	Ser	Ala	Ala	Val	Trp	Ser	Leu	Gly
			180					185					190		
Ile	Leu	Leu	Tyr	Asp	Met	Val	Cys	Gly	Asp	Ile	Pro	Phe	Glu	His	Asp
		195					200					205			
Glu	Glu	Ile	Ile	Arg	Gly	Gln	Val	Phe	Phe	Arg	Gln	Arg	Val	Ser	Ser
	210					215					220				
Glu	Cys	Gln	His	Leu	Ile	Arg	Trp	Cys	Leu	Ala	Leu	Arg	Pro	Ser	Asp
225					230					235					240
Arg	Pro	Thr	Phe	Glu	Glu	Ile	Gln	Asn	His	Pro	Trp	Met			
			245						250						

<210> 72  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:consensus  
 peptide

<400> 72  
 Asp Leu Phe Asp  
 1

<210> 73  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:consensus  
 peptide

<400> 73  
 Glu Asn Ile Leu  
 1

<210> 74  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide

<400> 74  
Val Trp Ser Leu Gly  
1 5

<210> 75  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
peptide

<400> 75  
Asn His Pro Trp  
1

<210> 76  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:5'-end  
32P-labeled oligonucleotide primer

<400> 76  
cactgactgt atg

13

<210> 77  
<211> 30  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Combined DNA/RNA  
Molecule:oligonucleotide template

<220>  
<223> Description of Artificial Sequence:oligonucleotide  
template

<400> 77  
ctcgtcagca tcttcaucat acagtcagtg

30

<210> 78  
 <211> 200  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:poly Gly  
 flexible linker

<220>

<221> MOD\_RES

<222> (6)..(200)

<223> Gly residues from position 6 to 200 may be present  
 or absent

<400> 78

Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
1				5					10					15			
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
			20					25					30				
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
		35					40					45					
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
	50					55				60							
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
65					70				75								80
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
			85					90						95			
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
		100						105					110				
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
	115						120					125					
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
	130					135					140						
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
145					150					155							160
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
		165						170							175		
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
	180							185						190			
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
	195							200									